

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Dumas Milne Edwards, J., et al.  
Application. No. : To be assigned  
Filed : Herewith  
For : **FULL-LENGTH HUMAN cDNAs ENCODING  
POTENTIALLY SECRETED PROTEINS**

1c406 U.S. PTO  
09/731872  
12/07/00

SEQUENCE SUBMISSION STATEMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

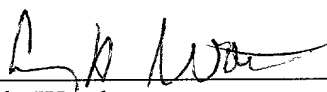
Dear Sir:

A copy of the Sequence Listing in computer readable form as required by 37 C.F.R.  
§ 1.821(e) is submitted herewith.

As required by 37 C.F.R. § 1.821(f), the data on the enclosed disk is identical to the  
Sequence Listing in the application filed herewith.

Respectfully submitted,

Dated: 12/7/00

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# SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste  
Bougueleret, Lydie  
Jobert, Severin

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Arg Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
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cccgctccgtg ccggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc      174
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Leu Leu Gly Pro Phe Ser Phe Leu Leu Val Leu Leu Val Thr
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Gly	Thr	Gly	Arg	Leu	Cys	Asp	Leu	Thr	Phe	Glu	Gln	Ile	Arg	Lys	Leu	
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Thr	Gly	Asp	Gly	Lys	Pro	Arg	Tyr	Asp	Thr	Phe	Trp	Lys	His	Phe	Ile	
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Phe	Val	Met	Met	Asp	Ile	Leu	Leu	Asp	Trp	Ser	Met	His	Asn	Ile	Leu	
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Leu	Gly	Ser	Ser	Tyr	Ile	Thr	Asp	Ser	Met	Val	Glu	Asp	Cys	Glu	Pro	
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Leu Val Ala Gly Gly Val Ala Gly Val Ser Val Asp Leu Ile Leu Phe
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cct ctg gat acc att aaa acc agg ctg cag agt ccc caa gga ttt agt 207
Pro Leu Asp Thr Ile Lys Thr Arg Leu Gln Ser Pro Gln Gly Phe Ser
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aag gct ggt ggt ttt cat gga ata tat gct ggc gtt cct tct gct gct 255
Lys Ala Gly Gly Phe His Gly Ile Tyr Ala Gly Val Pro Ser Ala Ala
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Lys His Met Leu Ala Ala Ser Ala Gly Glu Val Val Ala Cys Leu Ile
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Ser Trp Arg Gln Asp His Val Val Asp Ser Trp Gln Ser Ala Val Cys
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Gly Ala Phe Ala Gly Gly Phe Ala Ala Ala Val Thr Thr Pro Leu Asp
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Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe	Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	
			295			300					305					
tgg	gac	caa	cac	tac	ctc	agc	tgg	tcg	atg	ctc	ctg	ggg	gtg	ggc	ttc	1110
Trp	Asp	Gln	His	Tyr	Leu	Ser	Trp	Ser	Met	Leu	Leu	Gly	Val	Gly	Phe	

310	315	320	325	
cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg				1158
Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val				
	330	335	340	
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg				1206
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu				
	345	350	355	
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat				1248
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn				
	360	365	370	
taaggcccg c tctctggagg gaaggacatt actgaacctg tcttgctgtg cctcgaaact				1308
ctggagggtg gagcatcaag ttccagcccc cttcactccc ccatcttgct tttctgtgga				1368
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cttcttgcat ctccacacat ttcccttgga tgggacttgc aggcctaaat gagaggcatt				1548
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aaaaaaaaa aaaaa				1623

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 <222> 72..143

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 score 5.68931280801877  
 seq LGMLLGLLMAACT/PS

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Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala	
-15 -10 -5	
gcc tgc aca cct tct gcc tca gtc atc aga acc tgaaggagtt tgccctgacc	163
Ala Cys Thr Pro Ser Ala Ser Val Ile Arg Thr	
1 5	
aaccagaga agcagcac caaagaaacg gagagaaaag aaaccaaagc cgaggaggag	223
ctggatgctg aagtcctgga ggtgttccac ccgacgcatg agtggcaggc ccttcagcca	283
gggcaggctg tccctgcagg atcccacgta cggctgaatc ttcagactgg ggaaagagag	343
gcaaaactcc aatatgagga caagttccga aataatttga aaggcaaaag gctggatatc	403
aacaccaaca cctacacatc tcaggatctc aagagtgcac tggcaaaatt caaggagggg	463
gcagagatgg agagttcaaa ggaagacaag gcaaggcagg ctgagggtaaa gcggtctctc	523
cgccccattg aggaactgaa gaaagacttt gatgagctga atgttgctcat tgagactgac	583
atgcagatca tgggtacggct gatcaacaag ttcaatagtt ccagctccag tttggaagag	643
aagattgctg cgctctttga tcttgaatat tatgtccatc agatggacaa tgcgcaggac	703
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gtgaaggagt atgctgcgtt tgtgctgggc gctgcctttt ccagcaacct caaggtccag	823
gtggaggcca tcgaaggggg agccctgcag aagctgctgg tcatcctggc cacggagcag	883
ccgctcactg caaagggagg tgctcaccgt gcgcgtggtc aactgctct acgacctggt	943
cacggagaag atgttcgccg aggaggaggc tgagctgacc caggagatgt ccccagagaa	1003
gctgcagcag tatcgccagg tacacctcct gccakgcctg tgggaacagg gctggtgcga	1063
gatcacggcc cacctcctgg cgctgcccga gcatgatgcc ygtgagaagg tgctgcwgac	1123

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<222> 111..1154

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                                     Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu
      -25                               -20                               -15
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac 212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
      -10                               -5                               1                               5
ctg aag gag ttt gcc ctg acc aac cca gag aag agc agc acc aaa gaa 260
Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
      10                               15                               20
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
      25                               30                               35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
      40                               45                               50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
      55                               60                               65
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg 452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
      70                               75                               80                               85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat 500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
      90                               95                               100
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
      105                               110                               115
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596
Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg
      120                               125                               130
ccc att gag gaa ctg aag aaa gac ttt gat gag ctg aat gtt gtc att 644

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Pro	Ile	Glu	Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile		
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Glu	Thr	Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser		
150					155					160					165		
tcc	agc	tcc	agt	ttg	gaa	gag	aag	att	gct	gcg	ctc	ttt	gat	ctt	gaa	740	
Ser	Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu		
				170					175					180			
tat	tat	gtc	cat	cag	atg	gac	aat	gcg	cag	gac	ctg	ctt	tcc	ttt	ggg	788	
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	Gly		
			185					190					195				
ggg	ctt	caa	gtg	gtg	atc	aat	ggg	ctg	aac	agc	aca	gag	ccc	ctc	gtg	836	
Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	Leu	Val		
		200					205					210					
aag	gag	tat	gct	gcg	ttt	gtg	ctg	ggc	gct	gcc	ttt	tcc	agc	aac	ccc	884	
Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	Ser	Asn	Pro		
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Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	Gln	Lys	Leu	Leu		
		230			235				240					245			
gtc	atc	ctg	gcc	acg	gag	cag	ccg	ctc	act	gca	aag	aag	aag	gtc	ctg	980	
Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	Lys	Lys	Lys	Val	Leu		
			250						255					260			
ttt	gca	ctg	tgc	tcc	ctg	ctg	cgc	cac	ttc	ccc	tat	gcc	cag	cgg	cag	1028	
Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe	Pro	Tyr	Ala	Gln	Arg	Gln		
			265					270					275				
ttc	ctg	aag	ctc	ggg	ggg	ctg	cag	gtc	ctg	agg	acc	ctg	gtg	cag	gag	1076	
Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu	Arg	Thr	Leu	Val	Gln	Glu		
		280					285					290					
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Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val	Val	Thr	Leu	Leu	Tyr	Asp		
		295				300				305							
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Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu								
					315												
gatgtcccca	gagaagctgc	agcagtatcg	ccaggtacac	ctcctgccag	gcctgtggga											1234	
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 <222> 66..1256

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seq LLLRLRLNDAALRA/LQ

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    Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys
        -35                -30                -25
    ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
    Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
        -20                -15                -10
    gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
    Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
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    gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
    Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
        15                20                25
    ggt tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
    Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
        30                35                40
    ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct      350
    Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser
        45                50                55
    ggg cct aac agc ctc cac tgc ctg ggc tca ctc agg gag cgc ctc att      398
    Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile
        60                65                70                75
    att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga      446
    Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly
        80                85                90
    cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca      494
    His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr
        95                100                105
    gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta      542
    Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu
        110                115                120
    gag gag gtg tca gtg tca gat cca ctg gca agc aac caa gga cag tca      590
    Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser
        125                130                135
    ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc      638
    Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser
        140                145                150                155
    cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct      686
    Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser
        160                165                170
    gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act      734
    Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr
        175                180                185
    gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg cca agc      782
    Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser
        190                195                200
    ccc cta caa ggc ctg acc aat cag gat tta caa gag gga gaa gat tgg      830
    Pro Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp
        205                210                215
    gag caa gaa gat gag gac atg gac ccc aga tta gaa cac agt tcc tca      878
    Glu Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser
        220                225                230                235
    gtt caa gaa gat tct gaa tcc cca agt cct gaa gat ata cca gac tac      926
    Val Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr
        240                245                250

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gag cag gac ttt gag aca gat tat gct gaa tac cgc atc ctg cat gcc      1022
Glu Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala
      270                                275                                280
cgt gtt ggg act gca agc caa agg ttc ata gag ctg gga gca gag att      1070
Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile
      285                                290                                295
aaa aga gtt cgg cga gga act cca gaa tac aag gtc ctg gaa gac aag      1118
Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys
      300                                305                                310                                315
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Ile Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg
      320                                325                                330
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Glu Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile
      335                                340                                345
aaa ggt ctc atc ctg gag ttt gag gaa aag aac agg ggc agc
Lys Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser      1256
      350                                355                                360
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cgtccaggtg gcagagcagc taggaacgca aggcctgaac ctggggccag acaccctgct      180
ctcccggcc atg gtc aac gac cct cca gta cct gcc tta ctg tgg gcc cag      231
      Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln
      -20                                -15                                -10
gag gtg ggc caa gtc ttg gca ggc cgt gcc cgc agg ctg ctg ctg cag      279
Glu Val Gly Gln Val Leu Ala Gly Arg Ala Arg Leu Leu Leu Gln
      -5                                1                                5
ttt ggg gtg ctc ttc tgc acc atc ctc ctt ttg ctc tgg gtg tct gtc      327

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Phe	Gly	Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	
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Phe	Leu	Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	
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ctc	agc	cct	gtg	cat	ttc	tac	tac	agg	acc	gac	tgt	gat	tcc	tcc	acc	423
Leu	Ser	Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	
			45					50					55			
acc	tca	ctc	tgc	tcc	ttc	cct	gtt	gcc	aat	gtc	tcg	ctg	act	aag	ggc	471
Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	
		60					65					70				
gga	cgt	gat	cgg	gtg	ctg	atg	tat	gga	cag	ccg	tat	cgt	gtt	acc	tta	519
Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	
	75					80					85					
gag	ctt	gag	ctg	cca	gag	tcc	cct	gtg	aat	caa	gat	ttg	ggc	atg	ttc	567
Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	
	90				95				100					105		
ttg	gtc	acc	att	tcc	tgc	tac	acc	aga	ggc	ggc	cga	atc	atc	tcc	act	615
Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	
				110					115					120		
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Ser	Ser	Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	
			125					130					135			
ctg	gac	aca	ctg	gtc	ttc	tct	agc	ctc	ctg	cta	ttt	ggc	ttt	gca	gag	711
Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	
	140					145					150					
cag	aag	cag	ctg	ctg	gag	gtg	gaa	ctc	tac	gca	gac	tat	aga	gag	aac	759
Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	
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tcg	gtg	agt	gag	tac	gtg	ccg	acc	act	gga	gcg	atc	att	gag	atc	cac	807
Ser	Val	Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	
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agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	cgc	atc	cac	gcg	cac	855
Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	
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ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	ccg	atg	acc	tgc	gcc	903
Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	
			205					210					215			
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Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	
	220						225					230				
ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	tgg	ccc	cga	cac	cgc	999
Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	
	235				240						245					
ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	aat	tcc	cgg	aag	gaa	1047
Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	
	250				255					260					265	
gtc	caa	cga	agg	atc	tct	gct	cat	cag	cca	ggc	gca	ggg	cct	gaa	ggc	1095
Val	Gln	Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	
			270					275						280		
cag	gag	gag	tca	act	ccg	caa	tca	gat	gtt	aca	gag	gat	ggc	gag	agc	1143
Gln	Glu	Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	
			285					290					295			
cct	gaa	gat	ccc	tca	ggg	aca	gag	ggc	cag	ctg	tcc	gag	gag	gag	aaa	1191
Pro	Glu	Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	
	300						305					310				
cca	gat	cag	cag	ccc	ctg	agc	gga	gaa	gag	gag	cta	gag	cct	gag	gcc	1239
Pro	Asp	Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	

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315          320          325
agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg acg gag gcc 1287
Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala
330          335          340          345
aac ctg cct gct cct gct cct gct tct gct tct gcc cct gtc cta gag 1335
Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu
          350          355          360
act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga cag cgc ccc 1383
Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro
          365          370          375
acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc agcactttcc 1438
Thr Cys Ser Ser Ser
          380
cacctgactc ctctcccctc gtttttcctt caataaacta ttttgtgtca gctccaaaaa 1498
aaaaaaaaaa aa 1510

<210> 9
<211> 882
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..410

<220>
<221> sig_peptide
<222> 78..155
<223> Von Heijne matrix
      score 10.0731536331164
      seq LWLALVSCILTQA/SA

<400> 9
atggctggcc agaggaggaa cgctttgtgt tctcatcgga gctgcatggg aagtctgcat 60
acagcaaagt gacctgc atg cct cac ctt atg gaa agg atg gtg ggc tct 110
          Met Pro His Leu Met Glu Arg Met Val Gly Ser
          -25          -20
ggc ctc ctg tgg ctg gcc ttg gtc tcc tgc att ctg acc cag gca tct 158
Gly Leu Leu Trp Leu Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser
-15          -10          -5          1
gca gtg cag cga ggt tat gga aac ccc att gaa gcc agt tcg tat ggg 206
Ala Val Gln Arg Gly Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly
          5          10          15
ctg gac ctg gac tgc gga gct cct ggc acc cca gag gct cat gtc tgt 254
Leu Asp Leu Asp Cys Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys
          20          25          30
ttt gac ccc tgt cag aat tac acc ctc cta gat ttg ggg ccc atc act 302
Phe Asp Pro Cys Gln Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr
          35          40          45
cgg aga ggt gca cag tct ccc ggt gtc atg aat gga acc cct agc act 350
Arg Arg Gly Ala Gln Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr
          50          55          60          65
gca ggg ttc ctg gtg gcc tgg cct atg gtc ctc ctg act gtc ctc ctg 398
Ala Gly Phe Leu Val Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu
          70          75          80
gct tgg ctg ttc tgagagctcc gctgagcatc tggccttgaa gtttgtgttc 450
Ala Trp Leu Phe
          85

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gttggtgaag ggtaggcttt gttgaaaaag aaagaaagat tgaactacag gtgcatagca 1319
agcactcttt ctgggtaact aggctgctgg ttttaattac cctcagattt caccataaaa 1379
aacgcacaat tgtattatatt tacagagatg tgtccagcgc cccctgtggt gtgtgagaga 1439
aagcagctgc aactcaagtg actagggtggg cccagctggc ttcgtgcagg agggcacggt 1499
gggtgagcca ttctcgccat tctcatgtca gactgaaagg agggcctggg ccagctttga 1559
aaaggcagga tgaaatggaa aggtcaccac acttagggat ttttagacctt gactaacaag 1619
ctccagggtg agaaaaattc aaaacaaaat gtcaggaatc tagcagtgtt gtctgccctg 1679
gagcaaacaa acagtatgtg attttgcttc gcctatTTTT tttttctttt ttgggggaag 1739
ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
ataaatgaac ctttattaaa gacacttcaa tgcaaaaaaa aaaaaaaaaa 1849

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<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 55..468

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<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
      score 8.96936032049195
      seq FTLLFLAAVAGA/LV

```

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<400> 11
attccccaga ctttctgcag attctgtggt tatactcact cctcatccca aaga atg      57
                                                    Met
                                                    -15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc      105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
                        -10                        -5                        1
tat gct gaa gat gcc tcc tct gac tcg acg ggt gct gat cct gcc cag      153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
      5                        10                        15
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa      201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
      20                        25                        30
cca gct tca ccc cca gag aca acc aca aca gcc cag gag act tcg gcg      249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
      35                        40                        45                        50
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta      297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
                        55                        60                        65
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa      345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
                        70                        75                        80
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga      393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
                        85                        90                        95
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag      441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
      100                        105                        110
aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga      488
Lys Phe Ser Leu Leu Lys Pro Trp Ala
115                        120

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tcattggact taaagcctta aatacccttg tagcccagag ctattaaaac gaaagcatcc 548  
 aaaaaaaaaa aaaaaaa 565

<210> 12  
 <211> 1663  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 152..475

<220>  
 <221> sig\_peptide  
 <222> 152..244  
 <223> Von Heijne matrix  
 score 10.0910253445132  
 seq LVLLLVTRSPVNA/CL

<400> 12  
 atgtgtctgc tgccgccatt gtgcggcgct ggtccctca gagggttcct gctgctgccg 60  
 gtgccttgga ccctccccct cgcttctcgt tctactgccc caggagcccg gcgggtccgg 120  
 gactcccgtc cgtgccggtg cgggcgcggg c atg tgg ctg tgg gag gac cag 172  
 Met Trp Leu Trp Glu Asp Gln  
 -30 -25  
 ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg 220  
 Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu  
 -20 -15 -10  
 gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc 268  
 Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe  
 -5 1 5  
 gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc 316  
 Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala  
 10 15 20  
 ctg cag gtg ctc aag ccc ccg gac cgc att tct gcc atc gcc cac cgt 364  
 Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg  
 25 30 35 40  
 ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att ccg cag 412  
 Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln  
 45 50 55  
 cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg 460  
 Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu  
 60 65 70  
 acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgatgggac 515  
 Thr Gly Phe Leu Ser  
 75  
 tgggcgattg tgtgatttga catttgaaca aattaggaag ctgaatcctg cagcaaacca 575  
 cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaagggaag ctgttgcaga 635  
 gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac 695  
 tgaggctcta aagaaaatgt atatggaatt tcctcaactg tataataata gtgtggtctg 755  
 ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag 815  
 atgagacaaa cagatcggga tgtaataaca gcattaactc acagaccttg gagcctaagc 875  
 catacaggag atgggaaacc acgctatgat actttctgga aacattttat atttgttatg 935  
 atggacatth tgctcgattg gagcatgcat aatatcttgt ggtacctgtg tggaatttca 995  
 gctttcctca tgcaaaagga ttttgtatcc ccggcctact tgaagaagtg gtcagctaaa 1055  
 ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc 1115  
 catcttggtt ccagctatat cactgacagc atggtagaag actgcgaacc tcacttctag 1175  
 actttcacgg tgggacgaaa cgggttcaga aactgccagg ggccatcac agggatatca 1235

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aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
ttggtcactg catttttacc tgaaccaaag ctaaaccggg tgttgccacc atgcaccatg 1355
gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcattgataa ctcagagttg 1535
acattttaaa acttgccaca cttattttcaa atattttgtac tcagctatgt taacatgtac 1595
tntagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
aaaaaaaaa 1663

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<210> 13
<211> 744
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 112..552

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<220>
<221> sig_peptide
<222> 112..183
<223> Von Heijne matrix
      score 11.7298925418815
      seq FVLGLGLTPPTLA/QD

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<400> 13
tcacaactgg aacccatctc caggaacaaa cagctggaac ccattctccg ttgaagggaa 60
actgccagat ttttgtaaga ttcttctctc tgggagcctg tgttggaaga g atg gtg 117
                                     Met Val

atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
      -20              -15              -10

acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
      -5              1              5              10

acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
      15              20              25

gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
      30              35              40

aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
      45              50              55

aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
      60              65              70

tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
      75              80              85              90

cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
      95              100             105

tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg
      110             115             120

ccg taaccagcgg gcccttggtc aagtgtggc tctgtgtcc ttgccttcca 602
Pro

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tttcccctct gcacccagaa cagtgggtggc aacattcatt gccaaagggcc caaagaaaga 662
gctacctgga ccttttggtt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaa aaaaaaaaaa aa 744

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<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 101..1243

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<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57142340200611
      seq FLCLGMALCPRQA/TR

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<400> 14
gtagagtgct gaaggctctg ccaacggctc tcttggcgct tcaacgttcg gatcagcagc 60
ttttttccat tctctctctc cactttttca gtgagcagcc atg agt tgg act gtg 115
                                     Met Ser Trp Thr Val
                                     -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
      -25      -20      -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
      -10      -5      1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5      10      15      20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25      30      35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40      45      50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
      55      60      65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70      75      80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
85      90      95      100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
      105      110      115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
120      125      130
ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa 643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys
135      140      145

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ctg	att	att	gtt	tcc	aat	cca	gtg	gat	atc	tta	act	tat	gta	gct	tgg		691
Leu	Ile	Ile	Val	Ser	Asn	Pro	Val	Asp	Ile	Leu	Thr	Tyr	Val	Ala	Trp		
	150					155				160							
aag	ttg	agt	gca	ttt	ccc	aaa	aac	cgt	att	att	gga	agc	ggc	tgt	aat		739
Lys	Leu	Ser	Ala	Phe	Pro	Lys	Asn	Arg	Ile	Ile	Gly	Ser	Gly	Cys	Asn		
165					170				175					180			
ctg	gat	act	gct	cgt	ttt	cgt	ttc	ttg	att	gga	caa	aag	ctt	ggt	atc		787
Leu	Asp	Thr	Ala	Arg	Phe	Arg	Phe	Leu	Ile	Gly	Gln	Lys	Leu	Gly	Ile		
				185					190					195			
cat	tct	gaa	agc	tgc	cat	gga	tgg	atc	ctc	gga	gag	cat	gga	gac	tca		835
His	Ser	Glu	Ser	Cys	His	Gly	Trp	Ile	Leu	Gly	Glu	His	Gly	Asp	Ser		
			200					205					210				
agt	gtt	cct	gtg	tgg	agt	gga	gtg	aac	ata	gct	ggt	gtc	cct	ttg	aag		883
Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn	Ile	Ala	Gly	Val	Pro	Leu	Lys		
		215					220				225						
gat	ctg	aac	tct	gat	ata	gga	act	gat	aaa	gat	cct	gag	caa	tgg	aaa		931
Asp	Leu	Asn	Ser	Asp	Ile	Gly	Thr	Asp	Lys	Asp	Pro	Glu	Gln	Trp	Lys		
	230					235					240						
aat	gtc	cac	aaa	gaa	gtg	act	gca	act	gcc	tat	gag	att	att	aaa	atg		979
Asn	Val	His	Lys	Glu	Val	Thr	Ala	Thr	Ala	Tyr	Glu	Ile	Ile	Lys	Met		
245					250				255					260			
aaa	ggt	tat	act	tct	tgg	gcc	att	ggc	cta	tct	gtg	gcc	gat	tta	aca		1027
Lys	Gly	Tyr	Thr	Ser	Trp	Ala	Ile	Gly	Leu	Ser	Val	Ala	Asp	Leu	Thr		
				265				270					275				
gaa	agt	att	ttg	aag	aat	ctt	agg	aga	ata	cat	cca	gtt	tcc	acc	ata		1075
Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Arg	Ile	His	Pro	Val	Ser	Thr	Ile		
			280					285					290				
att	aag	ggc	ctc	tat	gga	ata	gat	gaa	gaa	gta	ttc	ctc	agt	att	cct		1123
Ile	Lys	Gly	Leu	Tyr	Gly	Ile	Asp	Glu	Glu	Val	Phe	Leu	Ser	Ile	Pro		
		295					300				305						
tgt	atc	ctg	gga	gag	aac	ggt	att	acc	aac	ctt	ata	aag	ata	aag	ctg		1171
Cys	Ile	Leu	Gly	Glu	Asn	Gly	Ile	Thr	Asn	Leu	Ile	Lys	Ile	Lys	Leu		
	310					315					320						
acc	cct	gaa	gaa	gag	gcc	cat	ctg	aaa	aaa	agt	gca	aaa	aca	ctc	tgg		1219
Thr	Pro	Glu	Glu	Glu	Ala	His	Leu	Lys	Lys	Ser	Ala	Lys	Thr	Leu	Trp		
325					330					335				340			
gaa	att	cag	aat	aag	ctt	aag	ctt	taaagttgcc	taaaactacc	attccgaaat							1273
Glu	Ile	Gln	Asn	Lys	Leu	Lys	Leu										
				345													

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<210> 15
<211> 1755
<212> DNA
<213> Homo sapiens
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<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57613483592743
      seq FLCLGMALCLRQA/TR

<400> 15
gtagagtgct gaaggtcctg ccaacggctc tcttggcgtc tcaacgttcg gatcagcagc      60
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg      115
                                   Met Ser Trp Thr Val
                                   -30
cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc      163
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe
      -25                                -20                                -15
cta tgc ctg ggg atg gcc ctg tgt ctg cgt caa gca acg cgc atc ccg      211
Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro
      -10                                -5                                1
ctc aac ggc acc tgg ctc ttc aca ccc gtg agc aag atg gcg act gtg      259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5                                10                                15                                20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac      307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25                                30                                35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct      355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40                                45                                50
atc agc atc ttg tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat      403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
      55                                60                                65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc      451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
      70                                75                                80
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg      499
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
85                                90                                95                                100
tca cag caa act cca acc tagtgattat cacagcaggt gcacgccaag      547
Ser Gln Gln Thr Pro Thr
      105
aaaagggaga aacgcgcctt aatttagtcc agcgaaatgt ggccatcttc aagtaatgat      607
ttccagtatt gtccagtaca gccccactg caaactgatt attgtttcca atccagtgga      667
tatcttaact tatgtagctt ggaagttgag tgcatttccc aaaaaccgta ttattggaag      727
cggctgtaat ctggatactg ctcgttttcg tttcttgatt ggacaaaagc ttggtatcca      787
ttctgaaagc tgccatggat ggatcctcgg agagcatgga gactcaagtg ttcctgtgtg      847
gagtggagtg aacatagctg gtgtcccttt gaaggatctg aactctgata taggaactga      907
taaatagctt gagcaggaaa aatgtccaca aagaagtgac tgcaactgcc tatgagatta      967
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gtattttgaa gaatcttagg agaatacatc cagtttccac cataactaag ggcctctatg      1087
gaatagatga agaagtattc ctcagtatcc cttgtatcct gggagagaaac ggtattacca      1147
accttataaa gataaagctg acccctgaag aagaggccca tctgaaaaaa agtgcaaaaa      1207
cactctggga aattcagaat aagcttaagc tttaaagttg cctaaaaacta ccattccgaa      1267
attattgaag agatcataga tacaggatta tataacgaaa ttttgaataa acttgaattc      1327
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aaagttagat taggtattt attgtgttct agaaattccg actcttttca ttagatatat      1567
gctattttct tcattcttgc tggtttatac ctatgttcat ttatatgctg taaaaaagta      1627
gtagcttctt ctacaatgta aaaataaatg tacatacaaa aaaatgcagt agtatatata      1687

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 Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys  
 -10 -5 1  
 agt agc act ttg aag cct act att gaa gca ttg cct aat gtg cta cct 154  
 Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro  
 5 10 15  
 tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act 202  
 Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr  
 20 25 30  
 ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat 250  
 Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp  
 35 40 45 50  
 ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct 298  
 Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser  
 55 60 65  
 gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346  
 Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn  
 70 75 80  
 gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394  
 Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala  
 85 90 95  
 ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac 442  
 Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His  
 100 105 110  
 cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490  
 Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro  
 115 120 125 130  
 gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg 538  
 Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met  
 135 140 145  
 acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg 586  
 Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu  
 150 155 160  
 tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct 634  
 Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser  
 165 170 175  
 gtc aac cca gag ctg gcc acg atg tct tac ttt cat cca tca gaa ggt 682

Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly		
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Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu		
195					200					205					210		
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Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu		
				215					220					225			
tct	aag	ata	atg	acg	gat	atc	att	tcc	ata	ggc	tca	gat	aat	gag	atg	826	
Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met		
			230					235					240				
cat	gaa	aac	gat	gag	tcg	ggt	acc	cgg	tgaagaaatc	aaggaacccg						873	
His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg									
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	Met	Asp	Ser	Ser	Thr	Ala	His	Ser	Pro	Val	Phe	Leu	Val				
	-20				-15					-10							
ttt	cct	cca	gaa	atc	act	gct	tca	gaa	tat	gag	tcc	aca	gaa	ctt	tca	159	
Phe	Pro	Pro	Glu	Ile	Thr	Ala	Ser	Glu	Tyr	Glu	Ser	Thr	Glu	Leu	Ser		
	-5				1				5								
gcc	acg	acc	ttt	tca	act	caa	agc	ccc	ttg	caa	aaa	tta	ttt	gct	aga	207	
Ala	Thr	Thr	Phe	Ser	Thr	Gln	Ser	Pro	Leu	Gln	Lys	Leu	Phe	Ala	Arg		
10				15				20				25					
aaa	atg	aaa	atc	tta	ggg	act	atc	cag	atc	ctg	ttt	gga	att	atg	acc	255	
Lys	Met	Lys	Ile	Leu	Gly	Thr	Ile	Gln	Ile	Leu	Phe	Gly	Ile	Met	Thr		
			30					35				40					
ttt	tct	ttt	gga	ggt	atc	ttc	ctt	ttc	act	ttg	tta	aaa	cca	tat	cca	303	
Phe	Ser	Phe	Gly	Val	Ile	Phe	Leu	Phe	Thr	Leu	Leu	Lys	Pro	Tyr	Pro		
		45				50					55						
agg	ttt	ccc	ttt	ata	ttt	ctt	tca	gga	tat	cca	ttc	tgg	ggc	tct	ggt	351	
Arg	Phe	Pro	Phe	Ile	Phe	Leu	Ser	Gly	Tyr	Pro	Phe	Trp	Gly	Ser	Val		
	60					65				70							
ttg	ttc	att	aat	tct	gga	gcc	ttc	cta	att	gca	gtg	aaa	aga	aaa	acc	399	
Leu	Phe	Ile	Asn	Ser	Gly	Ala	Phe	Leu	Ile	Ala	Val	Lys	Arg	Lys	Thr		
	75					80				85							
aca	gaa	act	ctg	ata	ata	ttg	agc	cga	ata	atg	aat	ttt	ctt	agt	gcc	447	
Thr	Glu	Thr	Leu	Ile	Ile	Leu	Ser	Arg	Ile	Met	Asn	Phe	Leu	Ser	Ala		

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90          95          100          105
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta      495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu

          110          115          120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag      543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

          125          130          135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc      591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe

          140          145          150
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc      639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys

          155          160          165
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata      692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys

170          175          180
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                        Met Ala Thr Ala Gln Leu Gln
                        -35
agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa      162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
      -30          -25          -20
cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc      210
His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
      -15          -10          -5
tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca      258
Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
1          5          10          15
aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat      306
Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
      20          25          30
tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat      354
Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp
      35          40          45
gct tta cag aaa aaa tat cta agg atg gtt gtt cta gct gta tac aca      402
Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val Leu Ala Val Tyr Thr
      50          55          60
aac cca gaa gat cct cag aca att tca gaa tgt tac caa ttc aaa ttc      450

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Lys	Tyr	Thr	Asn	Asn	Gly	Pro	Leu	Met	Asp	Phe	Ile	Ser	Lys	Asn	Gln	
				85					90					95		
agc	aac	gaa	tct	agc	atg	ttg	tct	act	gac	acc	aag	aaa	gca	agc	att	546
Ser	Asn	Glu	Ser	Ser	Met	Leu	Ser	Thr	Asp	Thr	Lys	Lys	Ala	Ser	Ile	
				100					105				110			
ctc	ctc	att	cgc	aag	att	tat	atc	cta	atg	caa	aat	ctg	ggg	cct	tta	594
Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile	Leu	Met	Gln	Asn	Leu	Gly	Pro	Leu	
				115					120				125			
cct	aat	gat	gtt	tgt	ttg	acc	atg	aaa	ctt	ttt	tac	tat	gat	gaa	gtt	642
Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys	Leu	Phe	Tyr	Tyr	Asp	Glu	Val	
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Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly	Phe	Lys	Asp	Gly	Asp	Cys	Glu	
145					150					155					160	
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Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met	Tyr	Leu	Asn	Val	Gly	Glu	Val	
				165						170					175	
tca	aca	cct	ttt	cac	atc	ttc	aaa	gta	aaa	gtg	acc	act	gag	aga	gaa	786
Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val	Lys	Val	Thr	Thr	Glu	Arg	Glu	
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cga	atg	gaa	aat	att	gac	tca	act	ata	cta	tca	cca	aaa	caa	ata	aaa	834
Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile	Leu	Ser	Pro	Lys	Gln	Ile	Lys	
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Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp	Lys	Asp	Val	Glu	Asp	Glu	Gln	
				210					215				220			
gag	cat	tat	aca	agt	gat	gat	ttg	gac	att	gaa	act	aaa	atg	gaa	gaa	930
Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp	Ile	Glu	Thr	Lys	Met	Glu	Glu	
225					230					235					240	
cag	gaa	aaa	aac	cct	gca	tct	tct	gaa	ctt	gaa	gaa	cca	agt	tta	gtt	978
Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu	Leu	Glu	Glu	Pro	Ser	Leu	Val	
				245					250					255		
tgt	gag	gaa	gat	gaa	att	atg	agg	tct	aaa	gaa	agt	cca	gat	ctt	tct	1026
Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser	Lys	Glu	Ser	Pro	Asp	Leu	Ser	
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att	tct	cat	tct	cag	gtt	gag	cag	tta	gtc	aat	aaa	aca	tct	gaa	ctt	1074
Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu	Val	Asn	Lys	Thr	Ser	Glu	Leu	
				275					280				285			
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Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser	Gly	Lys	Val	Phe	Gln	Asn	Lys	
				290					295			300				
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Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys	Ser	Ser	Lys	Glu	Asn	Arg	Lys	
305					310					315					320	
aga	agt	caa	cat	gaa	tct	ggg	aga	ata	gtc	ctc	cat	cac	ttt	gat	tct	1218
Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile	Val	Leu	His	His	Phe	Asp	Ser	
				325					330					335		
tct	agt	caa	gag	tca	gtg	cca	aaa	agg	aga	aag	ttt	agt	gaa	cca	aag	1266
Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg	Arg	Lys	Phe	Ser	Glu	Pro	Lys	
				340					345				350			
gaa	cat	ata	taaaaatttat	ttttgttctg	caggcttgca	gagttcttct										1315
Glu	His	Ile														
				355												
caccattttaa	actgaaggac	cctatatattat	atttccctaa	ctctgaagat	gtatatgtag											1375
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ttggattata aatttgggat tgattcactt tttacttatg ttaaaattat accatttaac 1675
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                                         -15
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Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
-10 -5 1
gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca 152
Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
5 10 15 20
gtt gca gaa agc aga aat ctg tat ata ttt gcg gat gaa tta cat ctg 200
Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
25 30 35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
40 45 50
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
55 60 65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
70 75 80
gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
85 90 95 100
tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat 440
Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
105 110 115
cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga 488
Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly
120 125 130
tta tta tct tct agt cca aac ttg ctc tgagctaaag gagaaatgga 535
Leu Leu Ser Ser Ser Pro Asn Leu Leu

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135          140
aacttgaagc tgggtgttatg tattttgcag gaaaacagtt tcatttttttc atagcaaaaa 595
tatagtgggt gtatatctct ccttaagtct ctgggtttcta aaaaccctac ttcagtaaag 655
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ggggcaagcc tgcaagcacg catcactggg gatctgacat gacaatggcc gcctgcccc 180
tctgagggct acaggactta cccagtgagg aagcagctaa gcaggtctga ccagccgacc 240
tggacctggc caagggtcct gtcacccctc atg gcc acc ccg cca ttc cgg ctg 294
                                Met Ala Thr Pro Pro Phe Arg Leu
                                -30 -25

ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc 342
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala
                                -20 -15 -10

tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa 390
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys
                                -5 1 5

cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa 438
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys
                                10 15 20

att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc 486
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe
25 30 35 40

cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa 534
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu
                                45 50 55

gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa 582
Glu Glu Arg Pro Phe Trp Glu Glu Glu Lys Thr Phe Trp Lys Glu Glu
                                60 65 70

aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act 630
Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr
                                75 80 85

ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg 678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp
90 95 100

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105                      110                      115                      120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
                      125                      130                      135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
                      140                      145                      150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
                      155                      160                      165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
                      170                      175                      180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185                      190                      195                      200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccagggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcctgaggca aggtttggaa aaccaaaaaa aaaaaaaaaa      1138

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<210> 21
<211> 468
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 76..276

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<220>
<221> sig_peptide
<222> 76..135
<223> Von Heijne matrix
      score 5.21332530399231
      seq SPVFLVFPPEITA/SE

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<400> 21
agcacaagaa aagaacatgg tctagactga agtaccaact aaatcatctc ctttcaaatt      60
atcaccgaca ccatac atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
      -20                      -15                      -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
      -5                      1                      5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
      10                      15                      20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
      25                      30                      35                      40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser
      45
ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc      366
ctttctcaat tttgggggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag      426

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cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa

468

<210> 22  
<211> 720  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 6..287

<220>  
<221> sig\_peptide  
<222> 6..80  
<223> Von Heijne matrix  
score 4.17710408129886  
seq ISLSHLFLDLSRS/LW

<400> 22  
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50  
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu  
-25 -20 -15  
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98  
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys  
-10 -5 1 5  
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146  
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu  
10 15 20  
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194  
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val  
25 30 35  
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242  
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu  
40 45 50  
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287  
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser  
55 60 65  
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaa 347  
atagtaagta aaatcttgct tgcctctcag taaaataaag ctctatTTTT cgtttttttt 407  
ttttccaact tcctgtacaa aaaagggaaa acttttagctt ttgggggaaa ttgggagcta 467  
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527  
aatactttat aaagatatatt tcataaatta cagcaatcct ggcttttagat gattgatggc 587  
cattttttaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647  
gtttcttaga aagtctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707  
aaaaaaaaaa aaa 720

<210> 23  
<211> 727  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 171..692

<220>  
<221> sig\_peptide  
<222> 171..227

<223> Von Heijne matrix  
 score 4.17573075349936  
 seq LLLGQRCSLKVSG/QE

<400> 23  
 attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggtc cctgggtctcc 60  
 tgggactact agccctttgt tgatagggag aagccaacat ctcccgcagg accccctaata 120  
 cttcagggca gctcccagag catggatccc tcctgattcc actcagcccg atg ttc 176  
 Met Phe  
 ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca 224  
 Leu Thr Val Lys Leu Leu Leu Gln Arg Cys Ser Leu Lys Val Ser  
 -15 -10 -5  
 ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg 272  
 Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu  
 1 5 10 15  
 aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg 320  
 Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu  
 20 25 30  
 gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct 368  
 Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser  
 35 40 45  
 atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc 416  
 Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala  
 50 55 60  
 cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta 464  
 His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu  
 65 70 75  
 gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta 512  
 Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu  
 80 85 90 95  
 agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg 560  
 Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu  
 100 105 110  
 gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca 608  
 Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro  
 115 120 125  
 gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt 656  
 Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys  
 130 135 140  
 gac atg gag gag aag gag gag gca gca gct gat cag taaacggggc 702  
 Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln  
 145 150 155  
 atcctaccgc aaaaaaaaaa aaaaa 727

<210> 24  
 <211> 470  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 137..454

<220>  
 <221> sig\_peptide  
 <222> 137..187  
 <223> Von Heijne matrix  
 score 10.7019149919754

seq VLMLLAVLIWTGA/EN

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atcctgtgaa ctacccaaaa ggaggaaaac gaacgcagct gagcatggga tgccatataa    60
aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc    120
tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg    172
          Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
                    -15                    -10
att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg    220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5                    1                    5                    10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg    268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
          15                    20                    25
tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat    316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
          30                    35                    40
cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt    364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
          45                    50                    55
ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc    412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
60                    65                    70                    75
atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt    454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
          80                    85
taaaaaaaaa aaaaaa    470

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<210> 25  
 <211> 987  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 238..609

<220>  
 <221> sig\_peptide  
 <222> 238..291  
 <223> Von Heijne matrix  
 score 10.0374888212272  
 seq LLLLVMALPPGTT/GV

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<400> 25
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agagggacgc agggcgttg gaacagagga cactccaggc gctgaccctg ggaggccagg    120
accagggcca aagtcccgtg ggcaagagga gtcctcagag gtccttcatt cagcggttcc    180
gggaggtctg ggaagccac ggccctggctg gggcagggtc aacgccgcca ggccgcc    237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc    285
Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
          -15                    -10                    -5
acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg    333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
          1                    5                    10
cag tgt cct ggt acc tac atg cac tgt ggc gat gac gag gac tgc ttc    381
Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
15                    20                    25                    30

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aca ggc cac ggg gtc gcc ccg ggc act ggt ccg gtc atc aac aaa ggc      429
Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
          35                      40                      45
tgc ctg cga gcc acc agc tgc ggc ctt gag gaa ccc gtc agc tac agg      477
Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
          50                      55                      60
ggc gtc acc tac agc ctc acc acc aac tgc tgc acc ggc cgc ctg tgt      525
Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
          65                      70                      75
aac aga gcc ccg agc agc cag aca gtg ggg gcc acc acc agc ctg gca      573
Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
          80                      85                      90
ctg ggg ctg ggt atg ctg ctt cct cca cgt ttg ctg tgaccaacag      619
Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
          95                      100                      105
ggaggacagg gcctgggact gttctcccag atccgccact ccccatgtcc ccatgtcctt      679
ccccactaa atggccagag aggccctgga caacctcttg cggccctggc ttcacccctt      739
ctaaggctgt ccaccaggag cccggtgcta ggggaagcat cccagggcct gactgagcgg      799
caggggagca cggcccggtg gtttgattgt attactctgt tccactgggt ctaagacgca      859
gagcttctca catctcaatc aggatgcttc tctccattgg tagcacttta gattccatga      919
aatatggtaa aaaatatata tatatcataa taaatgacag ctgatgttca tggaaaaaaaa      979
aaaaaaaaa

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<210> 26
<211> 908
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 80..862

<220>
<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.66725851505537
      seq FSLLSISGPPPISS/SA

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<400> 26
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta      60
ccccgcagtg ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga      112
              Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly
              -15                      -10
cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc      160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe
-5                      1                      5                      10
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act      208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr
          15                      20                      25
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc      256
Glu Ala Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile
          30                      35                      40
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc      304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser
          45                      50                      55
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc      352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile

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60		65		70		75	
tac cgg ccc tgg ttc tcc ccc tac agc tac ttc gtg tgt gca gac aaa							400
Tyr Arg Pro Trp Phe Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys							
	80		85		90		
gag agc cag ctg gag gcc tat gac ttc cca gag gtg cag cag gat gag							448
Glu Ser Gln Leu Glu Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu							
	95		100		105		
ggc aag tgg gac aac tgc ctt tct gag gac atg gct gag aac atc tgt							496
Gly Lys Trp Asp Asn Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys							
	110		115		120		
tcg tcc tct tcc tcc cca gag aac act tgc cct cga gaa gcc acc aag							544
Ser Ser Ser Ser Ser Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys							
	125		130		135		
aaa tcc agg cat ggc ctg gac tcc atc aca tcc cag gac atc cta atg							592
Lys Ser Arg His Gly Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met							
	140		145		150		155
gct tcc aga tgg cac cca gca cag cag aat ggc tac aag tgc gtg gcc							640
Ala Ser Arg Trp His Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala							
	160		165		170		
tgc tgc cgc atg tac ccc acc ctg gac ttc ctc aag agc cac atc aag							688
Cys Cys Arg Met Tyr Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys							
	175		180		185		
agg ggc ttc agg gag ggc ttc agc tgc aag gtg tac tac cgc aag ctc							736
Arg Gly Phe Arg Glu Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu							
	190		195		200		
aaa gcc ctc tgg agc aag gag cag aag gcc cgg ctg gga gac agg ctc							784
Lys Ala Leu Trp Ser Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu							
	205		210		215		
tcc tcc ggc agc tgc cag gcc ttc aat agt cct gct gaa cac ctt agg							832
Ser Ser Gly Ser Cys Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg							
	220		225		230		235
caa att ggc ggt gaa gcc tac tta tgt ctc tagagagatg ccaataaagt							882
Gln Ile Gly Gly Glu Ala Tyr Leu Cys Leu							
	240		245				
tagtcacagc caaaaaaaaaa aaaaaa							908

<210> 27

<211> 762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 83..310

<220>

<221> sig\_peptide

<222> 83..157

<223> Von Heijne matrix  
score 4.72955689475746  
seq LCALLSNFCPSTT/VK

<400> 27

ttttttctac tacaaacgcc atgggggatgc ggggtctggga acagcggaaa accctaccct 60

gccctgaaaa gtccctggct ca atg tgc atg tcc ctt tct atg aaa gtt cct 112

Met Cys Met Ser Leu Ser Met Lys Val Pro

-25 -20

tgc tgc cta tgc gcc ttg ctc tct aac ttc tgt ccc tcc aca act gtg 160

Cys	Cys	Leu	Cys	Ala	Leu	Leu	Ser	Asn	Phe	Cys	Pro	Ser	Thr	Thr	Val		
-15					-10					-5					1		
aaa	gga	gac	gtc	gtg	act	tcc	ttc	ttt	cgt	gct	gac	tat	gac	tta	gcc	208	
Lys	Gly	Asp	Val	Val	Thr	Ser	Phe	Phe	Arg	Ala	Asp	Tyr	Asp	Leu	Ala		
		5					10					15					
agt	agg	tct	gca	gat	cag	tcc	tcc	cag	aaa	gtg	aag	ttg	cgc	atg	ttc	256	
Ser	Arg	Ser	Ala	Asp	Gln	Ser	Ser	Gln	Lys	Val	Lys	Leu	Arg	Met	Phe		
		20				25					30						
act	ggg	cgt	ctt	ccc	atc	ggc	ccc	ttc	gcc	agt	gtg	ggg	aac	gcg	gcg	304	
Thr	Gly	Arg	Leu	Pro	Ile	Gly	Pro	Phe	Ala	Ser	Val	Gly	Asn	Ala	Ala		
	35				40					45							
gag	ctg	tgagccggcg	actcgggtcc	ctgaggtctg	gattctttct	ccgctactga										360	
Glu	Leu																
50																	
gacacggcgg	acacacacaa	acacagaacc	acacagccag	ttccaggagc	ccagtaatgg											420	
agagcccca	aaagaagaac	cagcagctga	aagtcgggat	cctacacctg	ggcagcagac											480	
agaagaagat	caggatacag	ctgagatccc	agtgcgcgac	atggaagggtg	atctgcaaga											540	
gctgcatcag	tcaaacaccg	gggataaatc	tggatttggg	ttccggcgctc	aagggtgaaga											600	
taatacctaa	agaggaacac	tgtaaaatgc	cagaagcagg	tgaagagcaa	ccacaagttt											660	
aaatgaagac	aagctgaaac	aacgcaagct	ggttttatat	tagatatattg	acttaaacta											720	
tctcaataaa	gttttgcagc	tttcacaaaa	aaaaaaaaaa	aa												762	

<210> 28  
 <211> 1102  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 310..906

<220>  
 <221> sig\_peptide  
 <222> 310..357  
 <223> Von Heijne matrix  
 score 11.0931109030915  
 seq FPLLLLSLGLVLA/EA

<400> 28																	
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gatcttttca	gttgagagac	ttcagctgtt	cattgctcat	ttggacttag	ttcaagggtca											120	
tgtcaaagaa	gaagggtgcac	ttacgctagt	tgtagctct	gtcttttgta	accatcaagt											180	
tccatgcgat	tgatcagatt	taggaggggg	cgttggggga	taatcaattt	tgggtgtcac											240	
caggtaaaca	gagccctcag	catctgaata	gaaactgaac	aggaacagaa	gagattcact											300	
acatctgag	atg gag acc	ttt cct ctg	ctg ctg ctg	ctc agc ctg	ggc ctg gtt											351	
	Met Glu Thr	Phe Pro Leu	Leu Leu Ser	Leu Gly Leu	Val												
	-15		-10		-5												
ctt gca gaa	gca tca gaa	agc aca atg	aag ata att	aaa gaa gaa	ttt											399	
Leu Ala Glu	Ala Ser Glu	Ser Thr Met	Lys Ile Ile	Lys Glu Glu	Phe												
	1		5		10												
aca gac gaa	gag atg caa	tat gac atg	gca aaa agt	ggc caa gaa	aaa											447	
Thr Asp Glu	Glu Met Gln	Tyr Asp Met	Ala Lys Ser	Gly Gln Glu	Lys												
	15		20		25				30								
cag acc att	gag ata tta	atg aac ccg	atc ctg tta	gtt aaa aat	acc											495	
Gln Thr Ile	Glu Ile Leu	Met Asn Pro	Ile Leu Leu	Val Lys Asn	Thr												
	35		40		45												
agc ctc agc	atg tcc aag	gat gat atg	tct tcc aca	tta ctg aca	ttc											543	
Ser Leu Ser	Met Ser Lys	Asp Asp Met	Ser Ser Thr	Leu Leu Thr	Phe												

	50		55		60	
aga agt tta cat tat aat gac	ccc aag gga aac agt tcg ggt aat gac	591				
Arg Ser Leu His Tyr Asn Asp	Pro Lys Gly Asn Ser Ser Gly Asn Asp					
65	70	75				
aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca	639					
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala						
80	85	90				
aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa	687					
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu						
95	100	105				
gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat	735					
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn						
115	120	125				
cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc	783					
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys						
130	135	140				
cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt	831					
Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val						
145	150	155				
acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg	879					
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met						
160	165	170				
agc tgg tta gtt tgt ggc tct aag ttg taaatccac agagcttttag	926					
Ser Trp Leu Val Cys Gly Ser Lys Leu						
175	180					
gactaggggtc ttactaaaga aggacctctt cttgttcatt cttgtttaaa cctttcctta		986				
atatctactc tttagcacta tagtgaactc ctgattattt attctaactg gaggagtga		1046				
aaatccaaaa ttgtggataa ttcaattaaa agttatgact gaaaaaaaaa aaaaaa		1102				

<210> 29  
 <211> 436  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 24..287

<220>  
 <221> sig\_peptide  
 <222> 24..131  
 <223> Von Heijne matrix  
 score 3.79790641648006  
 seq ILMRDFSPSGIFG/AF

<400> 29	
acagcggaca ccaggactcc aaa atg gcg tca gtt gta cca gtg aag gac aag	53
Met Ala Ser Val Val Pro Val Lys Asp Lys	
-35	-30
aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg	101
Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met	
-25	-20
cgg gac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac	149
Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr	
-10	-5
tac cgg tac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg	197
Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser	
10	15
	20

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ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt      245
Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
      25              30              35
tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac      287
Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
      40              45              50
tgaagaggac acactctgca cccccccacc ccacgacctt ggcccagagcc cctccgtgag      347
gaacacaatc tcaatcggtg ctgaatcctt tcatatccta ataggaatta acctccaaat      407
aaaacatgac tggtaaaaaa aaaaaaaaaa      436

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 <213> Homo sapiens

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 <222> 132..1574

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       seq LALLLTSTPEALG/AN

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ttggctactt aaggacctg ggcccaatcc acagctggga cagtcctggc ccaactgact      120
gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg      170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
      -25              -20              -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc      218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
      -10              -5              1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag      266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
      5              10              15              20
ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac      314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
      25              30              35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag      362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
      40              45              50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg      410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
      55              60              65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc      458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
      70              75              80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta      506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85              90              95              100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac      554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn
      105              110              115
ctc ctg ttg ggc agc gat tcc tcc ggg agg ccc aca gtt act gcc tcc      602
Leu Leu Leu Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser

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650  
 698  
 746  
 794  
 842  
 890  
 938  
 986  
 1034  
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 1178  
 1226  
 1274  
 1322  
 1370  
 1418  
 1466  
 1514

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ggg ctg cag atc cat aag gac ttc ctg ttc ttg ggt gcc aat gtc caa      1562
Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln
      440              445              450
tac atg aga gtt tgaggacaag aaagatgaag cttggagggtc acagctggat      1614
Tyr Met Arg Val
      455
ctgcttgttg catttccagc tgtgcagcac gtctcagaga ttcttgaaga atgaagacat      1674
ttctgctctc agctccgggg gtgaggtgtg cctggcctct gcctccaccc tcctcctctt      1734
caccaggtgc atgcatgccc tctctgagtc tggactttgc ttccccctcca ggaggggacca      1794
ccctccctga ctggcctggg atatctttac aagcaggcac tgtatttttt tattcgccat      1854
ctgatcccca tgcctagcag agtgctggca cttagtaggt cctcaataaa tatttattaa      1914
atgatgacaa aaaaaaaaaa aaaa      1938

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tgtcctctgt cgccgggaac tggcgaggta gttccttcgc ggtggagaga cctgga atg      119
                                     Met
gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca      167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
      -40              -35              -30
gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt      215
Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
      -25              -20              -15
ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat      263
Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
      -10              -5              1              5
caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa      311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
      10              15              20
cag ctt caa aca gaa cag gat gca cct gct gcc act cga cag cag ttc      359
Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe
      25              30              35
tac act gac atg tac tgt ccc atc tgc ctg cac caa gcc tcc ttc ccg      407
Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro
      40              45              50
gtg gag acc aac tgt gga cat ctt ttt tgt ggt gcc tgc att att gct      455
Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala
      55              60              65              70
tac tgg cga tat ggt tca tgg ctt ggg gca atc agt tgt cca atc tgt      503
Tyr Trp Arg Tyr Gly Ser Trp Leu Gly Ala Ile Ser Cys Pro Ile Cys
      75              80              85
aga caa acg aga cat ggc cac att gca ttg tcc aga aca gct      545

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Arg	Gln	Thr	Arg	His	Gly	His	Ile	Ala	Leu	Ser	Arg	Thr	Ala	
90			95			100								
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cagtatttgg	tgaagatgat	cagtctcagg	atgttctgag	attgcatcag	gatattaatg									665
attataaccg	gagattctca	gggcaaccca	gatctgtaag	taatgctaaa	gcatgttcaa									725
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tgactatgag	aaatcttggc	caggcacagt	agctaacgcc	tataatccta	gcactttggg									845
aggccaaggc	aggtggatca	cttgagccca	ggagtttgag	accagccttg	gaaacatgat									905
gaaaccccat	ctctagaaaa	aacaccaaaa	aattggacaa	gagtgttggc	acatgcctgt									965
agtccctgct	tcttgggagg	ctgaaatggg	aggatcacct	gagcccagga	ggttgaggct									1025
atagttagcc	atgatcgac	tattgcactc	ccacctgggt	ggcagtgaga	cccttctca									1085
aaaaacaaga	aaagaaaaaa	aaaaaaaaaa	a											1116

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tgctctctgt	cgccgggaac	tggcgaggta	gttccttcgc	ggtggagaga	cctgga atg									119
					Met									
					1									
gcc aaa tat	caa ggt gaa	ggt gtt caa	agt ttg aaa	ctg gat gat	gat tca									167
Ala Lys Tyr	Gln Gly Glu	Val Gln Ser	Leu Lys Leu	Asp Asp Asp	Ser									
	5	10	15											
ggt ata gaa	gga gta agc	gac caa gta	ctt gtg gca	ggt gtg gtc	agt									215
Val Ile Glu	Gly Val Ser	Asp Gln Val	Leu Val Ala	Val Val Val	Ser									
	20	25	30											
ttc gct ttg	att gct acc	ctg gta tat	gca ctt ttc	aga aat gta	cat									263
Phe Ala Leu	Ile Ala Thr	Leu Val Tyr	Ala Leu Phe	Arg Asn Val	His									
	35	40	45											
caa aac att	cac cca gaa	aac cag gag	cta gta agg	gta ctt cga	gaa									311
Gln Asn Ile	His Pro Gln	Asn Gln Glu	Leu Val Arg	Val Leu Arg	Glu									
	50	55	60	65										
cag ctt caa	aca gaa cag	gat gca cct	gct gac tcg	aca gca gtt	cta									359
Gln Leu Gln	Thr Glu Gln	Asp Ala Pro	Ala Asp Ser	Thr Ala Val	Leu									
	70	75	80											
cac tgacatgtac	tgtcccatct	gcctgcacca	agcctccttc	ccggtggaga										412
His														
ccaactgtgg	acatcttttt	tgtggtgcct	gcattattgc	ttactggcga	tatggttcat									472
ggcttggggc	aatcagttgt	ccaatctgta	gacaaacgag	acatggccac	attgcattgt									532
ccagaacagc	ttagaccatg	acagtttagca	tcgaagccac	ctgaggaggg	aggcagtaac									592
cttactccta	acagtatttg	gtgaagatga	tcagtctcag	gatgttctga	gattgcatca									652
ggatattaat	gattataaacc	ggagattctc	agggcaaccc	agatctgtaa	gtaatgctaa									712
agcatgttca	aagtttagagg	aagacacatt	tcttctcttt	tgtaaagtga	ggtttaccac									772
caagtattct	ttgactatga	gaaatcttgg	ccaggcacag	tagctaacgc	ctataatcct									832
agcacttttg	gaggccaagg	cagggtggatc	acttgagccc	aggagtttga	gaccagcctt									892
ggaaacatga	tgaaccccca	tctctagaaa	aaacaccaaa	aaattggaca	agagtgttgg									952
cacatgcctg	tagtccctgc	ttcttgggag	gctgaaatgg	gaggatcacc	tgagcccagg									1012
aggttgaggc	tatagtgagc	catgatcgca	ctattgcact	cccacctggg	tggcagtgag									1072
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 <222> 144..224  
 <223> Von Heijne matrix  
 score 5.14258625256317  
 seq FLCQRLVLSTLSG/RP

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 ccaccaccat cggagtcacg agtcccgcgt ctgtccgaag tcgccgtctt cgggctgctc 120  
 acgtctcttc ggagagcgcg cac atg gcg act cag gcg cac tcc ctc agc tac 173  
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr  
 -25 -20  
 gca ggg tgc aac ttc ttg tgc caa cgt ctg gtc ctg tct acc ctg agc 221  
 Ala Gly Cys Asn Phe Leu Cys Gln Arg Leu Val Leu Ser Thr Leu Ser  
 -15 -10 -5  
 ggg cgc ccc gtc aaa atc cga aag att cgg gcc aga gac gac aac ccg 269  
 Gly Arg Pro Val Lys Ile Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro  
 1 5 10 15  
 ggc ctc cga gat ttt gaa gcc agc ttc ata agg cta ttg gac aaa ata 317  
 Gly Leu Arg Asp Phe Glu Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile  
 20 25 30  
 acg aat ggt tct cga att gaa ata aac caa aca gga aca acc tta tat 365  
 Thr Asn Gly Ser Arg Ile Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr  
 35 40 45  
 tat cag cct ggc ctc ctg tat ggt gga tct gtg gaa cat gac tgt agc 413  
 Tyr Gln Pro Gly Leu Leu Tyr Gly Gly Ser Val Glu His Asp Cys Ser  
 50 55 60  
 gtc ctt cgt ggc att ggg tat tac ctg gag agt ctt ctt tgc ttg gct 461  
 Val Leu Arg Gly Ile Gly Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala  
 65 70 75  
 cca ttt atg aag cac ccg tta aaa ata gtt cta cga gga gtg acc aat 509  
 Pro Phe Met Lys His Pro Leu Lys Ile Val Leu Arg Gly Val Thr Asn  
 80 85 90 95  
 gat cag att gac cct tca gtt gat gtt ctt aag gca aca gca ctc cct 557  
 Asp Gln Ile Asp Pro Ser Val Asp Val Leu Lys Ala Thr Ala Leu Pro  
 100 105 110  
 ttg ttg aaa caa ttt ggg att gat ggt gaa tca ttt gaa ctg aag att 605  
 Leu Leu Lys Gln Phe Gly Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile  
 115 120 125  
 gtg cga cgg gga atg cct ccc gga gga gga ggc gaa gtg gtt ttc tca 653  
 Val Arg Arg Gly Met Pro Pro Gly Gly Gly Glu Val Val Phe Ser  
 130 135 140  
 tgt cct gtg agg aag gtc ttg aag ccc att caa ctc aca gat cca gga 701  
 Cys Pro Val Arg Lys Val Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly  
 145 150 155  
 aaa atc aaa cgt att aga gga atg gcg tac tct gta cgt gtg tca cct 749  
 Lys Ile Lys Arg Ile Arg Gly Met Ala Tyr Ser Val Arg Val Ser Pro  
 160 165 170 175  
 cag atg gcg aac cgg att gtg gat tct gca agg agc atc ctc aac aag 797

Gln Met Ala Asn Arg Ile Val Asp Ser Ala Arg Ser Ile Leu Asn Lys	
180	185
190	
ttc ata cct gat atc tat att tac aca gat cac att aaa gga gtc aac	845
Phe Ile Pro Asp Ile Tyr Ile Tyr Thr Asp His Ile Lys Gly Val Asn	
195	200
205	
tct ggg aag tct ccg ggc ttt ggg ttg tca ctg gtt gct gag acc acc	893
Ser Gly Lys Ser Pro Gly Phe Gly Leu Ser Leu Val Ala Glu Thr Thr	
210	215
220	
agt ggc acc ttc ctc agt gct gaa ctg gcc tcc aac ccc cag ggc cag	941
Ser Gly Thr Phe Leu Ser Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln	
225	230
235	
gga gca gca gta ctt cca gag gac ctt ggc agg aac tgt gcc cgg ctg	989
Gly Ala Ala Val Leu Pro Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu	
240	245
250	255
ctg ctg gag gaa atc tac agg ggt gga tgc gta gac tcg acc aac caa	1037
Leu Leu Glu Glu Ile Tyr Arg Gly Gly Cys Val Asp Ser Thr Asn Gln	
260	265
270	
agc ctg gcg cta cta ctc atg acc ctt gga cag cag gat gtt tcc aaa	1085
Ser Leu Ala Leu Leu Leu Met Thr Leu Gly Gln Gln Asp Val Ser Lys	
275	280
285	
gtc ctg cta ggc cct ctc tct ccc tac acg ata gaa ttt ttg cgg cat	1133
Val Leu Leu Gly Pro Leu Ser Pro Tyr Thr Ile Glu Phe Leu Arg His	
290	295
300	
ttg aag agc ttt ttc cag att atg ttt aaa att gaa acc aag cca tgt	1181
Leu Lys Ser Phe Phe Gln Ile Met Phe Lys Ile Glu Thr Lys Pro Cys	
305	310
315	
ggt gaa gaa ctc aag ggt ggg gat aaa gtg ctg atg acc tgt gtt ggc	1229
Gly Glu Glu Leu Lys Gly Gly Asp Lys Val Leu Met Thr Cys Val Gly	
320	325
330	335
att ggt ttc tcc aac ctt agc agg acc ctc aag tgataaccat cacaagataa	1282
Ile Gly Phe Ser Asn Leu Ser Arg Thr Leu Lys	
340	345
ggccccagtg cctacagaca aagcagaagc tgccacggac accaatggga ccaagtccaa	1342
atggattaat ccaggacaga atagccactt gcttaatttt ctgtgaagaa atatcaatat	1402
acaaataaaaa gacatccctg tagcatatgg tttccagctg tttctccagt ggcattgccaa	1462
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gccttcaggc cacagtcgtg ctgctagaac agtctcgtag ctgcagttca gctgtgcttc	1582
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gtcagaaatt ggtgtattag actatttatc tttgatcttc tgaatggatt gctgtcatgg	1822
acacggacac ggatcttcat ctgggttcatt gtatttatat gtgagggatg gatggctgcg	1882
gggctccaag taagtatttg ggatgttttt atattccagg tgtgctgtac gttcttattt	1942
tattttcaca atagctctgt gatgtaagtg ctatctccat gagaaaattc ataaaggggtg	2002
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aaaaaaaaa	2072

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 <211> 409  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 35..316

<220>  
 <221> sig\_peptide

<222> 35..109

<223> Von Heijne matrix

score 5.38058532480537

seq AVTSLLSPTPATA/LA

<400> 34

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                               Met Ala Ser Val Val Leu Ala
                               -25                               -20
ctg agg acc cgg aca gcc gtt aca tcc ttg cta agc ccc act ccg gct      103
Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala
          -15          -10          -5
aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc      151
Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
          1          5          10
aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa      199
Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
15          20          25          30
atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc      247
Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
          35          40          45
cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc      295
His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
          50          55          60
ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccctaa gcatggtaat      346
Pro Leu Phe Pro Phe Leu Gly
          65
aacagttgca tgtattgagt gcttaccaaaa tggcaagcat tgtgccaaaa aaaaaaaaaa      406
aaa                                                                409
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<211> 836

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 177..767

<220>

<221> sig\_peptide

<222> 177..236

<223> Von Heijne matrix

score 6.51720597568932

seq LAVILTLLGLAIL/AI

<400> 35

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acaccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct      120
ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg      179
                               Met
                               -20
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt      227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
          -15          -10          -5
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt      275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
          1          5          10
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gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg	323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu	
15 20 25	
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt	371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser	
30 35 40 45	
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg	419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu	
50 55 60	
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa	467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys	
65 70 75	
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg	515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met	
80 85 90	
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc	563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu	
95 100 105	
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct	611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro	
110 115 120 125	
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc	659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu	
130 135 140	
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc	707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser	
145 150 155	
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt	755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu	
160 165 170	
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg	807
Phe Ser Pro Ala	
175	
atagtgtata aatgaaaaaa aaaaaaaaaa	836

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<211> 1323

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 208..1239

<220>

<221> sig\_peptide

<222> 208..294

<223> Von Heijne matrix

score 5.73027134157378

seq GLVLICVCSKTHS/LK

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gctgctgttt gaattatctg tgaatgttgg gaagaggaat gccagagctg ccggctgaaa	180
attacccaac caagagaaat ctgcagg atg gac ttt ctg gtc ctc ttc ttg ttc	234
Met Asp Phe Leu Val Leu Phe Leu Phe	

-25

tac ctg gct tcg gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc tcg	282
Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys Ser	
-20 -15 -10 -5	
aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata ttt	330
Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile Phe	
1 5 10	
tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg ctt	378
Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu Leu	
15 20 25	
cat tac ctt ttc cat acg aga aac acc ttc att gtc ctg cac ctg	426
His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His Leu	
30 35 40	
gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt ggc	474
Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe Gly	
45 50 55 60	
tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc tat	522
Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro Tyr	
65 70 75	
ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga acc	570
Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly Thr	
80 85 90	
aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat gtt	618
Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His Val	
95 100 105	
tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct act	666
Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser Thr	
110 115 120	
tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt aac	714
Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys Asn	
125 130 135 140	
tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac tgc	762
Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn Cys	
145 150 155	
atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc ttg	810
Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu	
160 165 170	
acg gcc tcg gct gcc acc gtc gcc att gtg agc acc act ttt ctg gtc	858
Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu Val	
175 180 185	
cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat gac	906
His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp	
190 195 200	
ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac ctg	954
Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr Leu	
205 210 215 220	
ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg gtt	1002
Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val Val	
225 230 235	
ctg agc ttc ctc ctg ggt ggc tac ctg ttg ttt gtc ctg tat ctg gcg	1050
Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu Ala	
240 245 250	
gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc tgg	1098
Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala Trp	
255 260 265	
tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc caa	1146
Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro Ser Ala Glu Pro Gln	
270 275 280	
gtc cac cgg aac att cac tcc cat ggg ctt cgg agc aac ctt caa gag	1194





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gtt act gct gtt tgc gag gta ttc ctc tgc tgt gag cag ggc tgg cca 1547
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
      455                      460                      465
gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act 1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
      470                      475                      480
ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg 1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
485                      490                      495                      500
act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg 1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
      505                      510
gaagcctgga caccgcaggc acctggacca gctatgggta gttctgtggg tggaacacat 1752
tctgtgtaag agccccactg agggctctgc agcggagtga cagcaacccc agagatgagg 1812
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg 1872
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<213> Homo sapiens

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<220>
<221> CDS
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atcgatggta gctataagag tcgtgtctga acccggtctt tccaattggc ctgctccatc 180
cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg 230
      Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu
      -20                      -15
ctg ttg ctc ggc ccc ggg ctc ctg gcg acc gtg cgg gcc gaa tgc agc 278
Leu Leu Leu Gly Pro Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser
      -10                      -5                      1
cag gat tgc gcg acg tgc agc tac cgc cta gtg cgc ccg gcc gac atc 326
Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
      5                      10                      15
aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg 374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
20                      25                      30                      35
aaa att tgg gaa acc tgc aag gag ctc ctg cag ctg tcc aaa cca gat 422
Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
      40                      45                      50
ctt cct caa gat ggc acc agc acc ctc aga gaa aat agc aaa ccg gaa 470
Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu
      55                      60                      65
gaa agc cat ttg cta gcc aaa agg tat ggg gcc ttc atg aaa agg tat 518
Glu Ser His Leu Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr

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      70      75      80
gga ggc ttc atg aag aaa atg gat gag ctt tat ccc atg gag cca gaa      566
Gly Gly Phe Met Lys Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu
      85      90      95
gaa gag gcc aat gga agt gag atc ctc gcc aag cgg tat ggg ggc ttc      614
Glu Glu Ala Asn Gly Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe
100      105      110      115
atg aag aag gat gca gag gag gac gac tcg ctg gcc aat tcc tca gac      662
Met Lys Lys Asp Ala Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp
      120      125      130
ctg cta aaa gag ctt ctg gaa aca ggg gac aac cga gag cgt agc cac      710
Leu Leu Lys Glu Leu Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His
      135      140      145
cac cag gat ggc agt gat aat gag gaa gaa gtg agc aag aga tat ggg      758
His Gln Asp Gly Ser Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly
      150      155      160
ggc ttc atg aga ggc tta aag aga agc ccc caa ctg gaa gat gaa gcc      806
Gly Phe Met Arg Gly Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala
      165      170      175
aaa gag ctg cag aag cga tat ggg ggc ttc atg aga aga gta ggt cgc      854
Lys Glu Leu Gln Lys Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg
180      185      190      195
cca gag tgg tgg atg gac tac cag aaa cgg tat gga ggt ttc ctg aag      902
Pro Glu Trp Trp Met Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys
      200      205      210
cgc ttt gcc gag gct ctg ccc tcc gac gaa gaa ggc gaa agt tac tcc      950
Arg Phe Ala Glu Ala Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser
      215      220      225
aaa gaa gtt cct gaa atg gaa aaa aga tac gga gga ttt atg aga ttt      998
Lys Glu Val Pro Glu Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe
      230      235      240
taatattttt cccactagtg gccccaggcc ccagcaagcc tccctccatc ctccagtggg      1058
aaactgttga tgggtgtttta ttgtcatgtg ttgcttgcc tgtatagttg acttcattgt      1118
ctggataact atacaacctg aaaactgtca ttccagggtc tgtgctcttt ttggagtctt      1178
taagctcagt attagtctat tgcagctatc tcgttttcat gctaaaatag tttttgttat      1238
cttgtctctt atttttgaca aacatcaata aatgcttact tgtatataga gataataaac      1298
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 <213> Homo sapiens

<220>  
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 <222> 505..1590

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 score 8.5056444915604  
 seq VVMLMLLTLLVLG/MV

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gggcttcctt ggaggtaaag agctaggggtg ggggtggcagt gggtagaacc ccagctggac      180

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agctccttcc ttagctctgt gattgctaca gctggttctg gaagccacag gcgcctcag	240
gacaaatggg gcttcttcag cacagggtag tgagtgtga gctaagcaag gacactgtcc	300
ccttctctgc ccaggctcga gctgtgcacc tttaccctgg caattgccct ggggtgtgtc	360
ctgtctctgc ccttctccat catcagcaat gaggtgtgtc tctccctgcc tcggaactac	420
tacatccagt ggctcaacgg ctccctcatc catggcctct ggaaccttgt ttttctcttc	480
tccaacctgt cctcatctt cctc atg ccc ttt gca tat ttc ttc act gag	531
Met Pro Phe Ala Tyr Phe Phe Thr Glu	
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Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg Val Tyr	
-30 -25 -20	
gag aca gtg gtg atg ttg atg ctc ctc act ctg ctg gtg cta ggt atg	627
Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val Leu Gly Met	
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Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys Ala Asn Arg Glu	
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Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys	
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atc tcc ttc ctt ggg gtt ctg ctg ctc ctg gtg tgt act cca ctg ggt	771
Ile Ser Phe Leu Gly Val Leu Leu Leu Leu Val Cys Thr Pro Leu Gly	
35 40 45	
ctc gcc cgc atg ttc tcc gtc act ggg aag ctg cta gtc aag ccc cgg	819
Leu Ala Arg Met Phe Ser Val Thr Gly Lys Leu Leu Val Lys Pro Arg	
50 55 60 65	
ctg ctg gaa gac ctg gag gag cag ctg tac tgc tca gcc ttt gag gag	867
Leu Leu Glu Asp Leu Glu Glu Gln Leu Tyr Cys Ser Ala Phe Glu Glu	
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Ala Ala Leu Thr Arg Arg Ile Cys Asn Pro Thr Ser Cys Trp Leu Pro	
85 90 95	
tta gac atg gag ctg cta cac aga cag gtc ctg gct ctg cag aca cag	963
Leu Asp Met Glu Leu Leu His Arg Gln Val Leu Ala Leu Gln Thr Gln	
100 105 110	
agg gtc ctg ctg gag aag agg cgg aag gct tca gcc tgg caa cgg aac	1011
Arg Val Leu Leu Glu Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn	
115 120 125	
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Leu Gly Tyr Pro Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu	
130 135 140 145	
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Ser Val Leu Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu	
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Ala Ala Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser	
165 170 175	
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Phe Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile	
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Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro Leu	
195 200 205	
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Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr Gln Ile	
210 215 220 225	
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Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala Leu Pro Val	

ttc tct cga acc ctg ggg ctc act cgc ttt gac ctg ctg ggt gac ttt	230	235	240	1395
Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu Leu Gly Asp Phe				
gga cgc ttc aac tgg ctg ggc aat ttc tac att gtg ttc ctc tac aac	245	250	255	1443
Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile Val Phe Leu Tyr Asn				
gca gcc ttt gca ggc ctc acc aca ctc tat ctg gtg aag acc ttc act	260	265	270	1491
Ala Ala Phe Ala Gly Leu Thr Thr Leu Tyr Leu Val Lys Thr Phe Thr				
gca gct gtg cgg gca gag ctg atc cgg gcc ttt ggg ctg gac aga ctg	275	280	285	1539
Ala Ala Val Arg Ala Glu Leu Ile Arg Ala Phe Gly Leu Asp Arg Leu				
ccg ctg ccc gtc tcc ggt ttc ccc cag gca tct agg aag acc cag cac	290	295	300	1587
Pro Leu Pro Val Ser Gly Phe Pro Gln Ala Ser Arg Lys Thr Gln His				
cag tgacctccag ctgggggtgg gaagaaaaaa actggacact gccatctgct	310	315	320	1640
Gln				
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cagagcctaa gcaactgtgct atcctggagg ggctttggac cacctgaaag accaagggga				2060
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 score 6.39000252120129  
 seq LGLSVLLTAATVA/GV

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aggccgcggc cgccagcgtg ggg atg tct agg agc tcg aag gtg gtg ctg ggc		113
Met Ser Arg Ser Ser Lys Val Val Leu Gly		
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ctc tcg gtg ctg ctg acg gcg gcc aca gtg gcc ggc gta cat gtg aag		161
Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val Lys		
-10	-5	1
cag cag tgg gac cag cag agg ctt cgt gac gga gtt atc aga gac att		209
Gln Gln Trp Asp Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile		
10	15	20
gag agg caa att cgg aaa aaa gaa aac att cgt ctt ttg gga gaa cag		257
Glu Arg Gln Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln		
25	30	35

att att ttg act gag caa ctt gaa gca gaa aga gag aag atg tta ttg 305  
Ile Ile Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu  
40 45 50

gca aaa gga tct caa aaa tca tgacttgaat gtgaaatattc tgttggacag 356  
Ala Lys Gly Ser Gln Lys Ser  
55 60

acaacacgag tttgtgtgtg tgtgttgatg gagagtagct tagtagtatc ttcattctttt 416  
tttttgggtca ctgtcctttt aaacttgatc aaataaagga cagtgggtca tataagttac 476  
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seq SGLLLQVLFRLIT/FV

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Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly  
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Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val  
10 15 20

aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc 250  
Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala  
25 30 35

ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc cag 298  
Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln  
40 45 50

acc ctc aac ctg ctg tgg cta aca gtc ccc ctg ggt gtg ttt tgg tcc 346  
Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp Ser  
55 60 65

tta ttc ctg ggc tgg atc tgg ttg cag ctg ctt gaa gtg cct gat cct	394
Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp Pro	
70 75 80 85	
aat gtt gtc cct cac tat gca act gga gtg gtg ctg ttt ggt ctc tcg	442
Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu Ser	
90 95 100	
gca gtg gtg gag ctt cta gga gag ccc ttt tgg gtc ttg gca caa gca	490
Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln Ala	
105 110 115	
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His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val Ile	
120 125 130	
ctt aag agc gtt ctg aca gct ttt ctc gtg ctg tgg ttg cct cac tgg	586
Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His Trp	
135 140 145	
gga ttg tac att ttc tct ttg gcc cag ctt ttc tat acc aca gtt ctg	634
Gly Leu Tyr Ile Phe Ser Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu	
150 155 160 165	
gtg ctc tgc tat gtt att tat ttc aca aag tta ctg ggt tcc cca gaa	682
Val Leu Cys Tyr Val Ile Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu	
170 175 180	
tca acc aag ctt caa act ctt cct gtc tcc aga ata aca gat ctg tta	730
Ser Thr Lys Leu Gln Thr Leu Pro Val Ser Arg Ile Thr Asp Leu Leu	
185 190 195	
ccc aat att aca aga aat gga gcg ttt ata aac tgg aaa gag gct aaa	778
Pro Asn Ile Thr Arg Asn Gly Ala Phe Ile Asn Trp Lys Glu Ala Lys	
200 205 210	
ctg act tgg agt ttt ttc aaa cag tct ttc ttg aaa cag att ttg aca	826
Leu Thr Trp Ser Phe Phe Lys Gln Ser Phe Leu Lys Gln Ile Leu Thr	
215 220 225	
gaa ggc gag cga tat gtg atg aca ttt ttg aat gta ttg aac ttt ggt	874
Glu Gly Glu Arg Tyr Val Met Thr Phe Leu Asn Val Leu Asn Phe Gly	
230 235 240 245	
gat cag ggt gtg tat gat ata gtg aat aat ctt ggc tcc ctt gtg gcc	922
Asp Gln Gly Val Tyr Asp Ile Val Asn Asn Leu Gly Ser Leu Val Ala	
250 255 260	
aga tta att ttc cag cca ata gag gaa agt ttt tat ata ttt ttt gct	970
Arg Leu Ile Phe Gln Pro Ile Glu Glu Ser Phe Tyr Ile Phe Phe Ala	
265 270 275	
aag gtg ctg gag agg gga aag gat gcc aca ctt cag aag cag gag gac	1018
Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu Asp	
280 285 290	
gtt gct gtg gct gct gca gtc ttg gag tcc ctg ctc aag ctg gcc ctg	1066
Val Ala Val Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala Leu	
295 300 305	
ctg gcc ggc ctg acc atc act gtt ttt ggc ttt gcc tat tct cag ctg	1114
Leu Ala Gly Leu Thr Ile Thr Val Phe Gly Phe Ala Tyr Ser Gln Leu	
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gct ctg gat atc aac gga ggg acc atg ctt agc tca gga tcc ggt cct	1162
Ala Leu Asp Ile Asn Gly Gly Thr Met Leu Ser Ser Gly Ser Gly Pro	
330 335 340	
gtt ttg ctg cgt tcc tac tgt ctc tat gtt ctc ctg ctt gcc atc aat	1210
Val Leu Leu Arg Ser Tyr Cys Leu Tyr Val Leu Leu Leu Ala Ile Asn	
345 350 355	
gga gtg aca gag tgt ttc aca ttt gct gcc atg agc aaa gag gag gtc	1258
Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu Val	
360 365 370	
gac agg tac aat ttt gtg atg ctg gcc ctg tcc tcc tca ttc ctg gtg	1306

Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val		
375						380				385							
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Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu		
390					395				400						405		
gcc	aac	tgc	ttt	aac	atg	ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	1402	
Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe		
				410					415					420			
atc	cac	cgc	tac	tac	cga	agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	1450	
Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu		
			425					430					435				
cac	cta	tgc	cca	gtc	ctg	ctc	ggg	aca	ttt	gcc	ctc	agt	ggt	ggg	gtt	1498	
His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val		
			440				445					450					
act	gct	gtt	tgc	gag	gta	ttc	ctc	tgc	tgt	gag	cag	ggc	tgg	cca	gcc	1546	
Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp	Pro	Ala		
			455			460					465						
aga	ctg	gca	cac	att	gct	gtg	ggg	gcc	ttc	tgt	ctg	gga	gca	act	ctc	1594	
Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu		
470					475					480					485		
ggg	aca	gca	ttc	ctc	aca	gag	acc	aag	ctg	atc	cat	ttc	ctc	agg	act	1642	
Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	Thr		
				490					495					500			
cag	tta	ggt	gtg	ccc	aga	cgc	act	gac	aaa	atg	acg	tgacttcagg				1688	
Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr						
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gaagcctgga	cacccgaggc	acctggacca	gctatgggta	gttctgtggg	tggaacacat											1748	
tctgtgtaag	agccccactg	agggctctgc	agcggagtga	cagcaacccc	agagatgagg											1808	
caccagagag	tgccactgca	tgagacacct	gtgaccattc	gaagtctgaa	atgcgggggg											1868	
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tatagtgaaa	aaaaaaaaaaa	aaaaaa														1953	

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<211> 1688

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<213> Homo sapiens

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<222> 119..1522

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<221> sig\_peptide

<222> 119..181

<223> Von Heijne matrix  
score 11.6921972463885  
seq LLLCLALSGAET/KP

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atg ggc aca	cag gag ggc	tgg tgc ctg	ctg ctg ctc	tgc ctg gct	cta tct	166	
Met Gly Thr	Gln Glu Gly	Trp Cys Leu	Leu Leu Leu	Cys Leu Ala	Leu Ser		
-20		-15		-10			
gga gca gca	gaa acc aag	ccc cac cca	gca gag ggg	cag tgg cgg	gca	214	
Gly Ala Ala	Glu Thr Lys	Pro His Pro	Ala Glu Gly	Gln Trp Arg	Ala		
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gtg gac gtg	gtc cta gac	tgt ttc ctg	gtg aag gac	ggt gcg cac	cgt	262	



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          320          325          330
tcc agc ctc agg caa agc gtg gca ggc acc tac agc atc tcc tcc tct      1222
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
          335          340          345
ctc acc gca gaa cct ggc tct gca ggt gcc act tac acc tgc cag gtc      1270
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
          350          355          360
aca cac atc tct ctg gag gag ccc ctt ggg gcc agc acc cag gtt gtc      1318
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
          365          370          375
cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc      1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
380          385          390          395
ttc ctt ctt gca ctg atg ttc ctg ggg ctt cag aga cgg caa gca cct      1414
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
          400          405          410
aca gga ctt ggg ctg ctt cag gct gaa cgc tgg gag acc act tcc tgt      1462
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
          415          420          425
gct gac aca cag agc tcc cat ctc cat gaa gac cgc aca gcg cgt gta      1510
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
          430          435          440
agc cag ccc agc tgacctaaag cgacatgaga ctactagaaa gaaacgacac      1562
Ser Gln Pro Ser
          445
ccttccccaa gccccacag ctactccaac ccaaacaaca accaagccag tttaatggta      1622
ggaatttgta ttttttgct ttgttcagaa tacatgacat tggtaaataa aaaaaaaaaa      1682
aaaaaa      1688

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<222> 334..1551

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<221> sig_peptide
<222> 334..426
<223> Von Heijne matrix
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      seq TVFLLVTLQALDT/VE

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agactgcatg ctgcttcctc tcgatgccaa gccagacctt ctcacaacct cggatctcag      180
tccttcatgg agacctggtc ccagcaggaa tggcagtgca ggaaattggc gcccagatgg      240
ttcttccatg tgaagttgtc tcgggctctg ggctgacgag agaacacctg gtaaccaggt      300
tagccctctg tcagtcaccc agggcagggc agc atg gtg cgg att cag agg agg      354
      Met Val Arg Ile Gln Arg Arg
      -30          -25
aag ctt ttg gca tct tgc ctg tgc gtc aca gcc acc gtc ttt ctg ctt      402
Lys Leu Leu Ala Ser Cys Leu Cys Val Thr Ala Thr Val Phe Leu Leu
      -20          -15          -10
gtc aca ctc cag gcc ttg gat acc gtt gag aat cta atg aaa gtc acg      450

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	300		305		310	
gtc cct gta tat tac gga tcc ccc agc atc aca gac tgg ctt cca agt						1410
Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser						
	315		320		325	
aac aaa agt gct att ctt gta tca gaa ttt tct cac ccc agg gaa ctg						1458
Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu						
	330		335		340	
gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc						1506
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala						
	345		350		355	360
tat gta gaa tgg aag ctg aag ggt aga tct cta acc agc gac ttc						1551
Tyr Val Glu Trp Lys Leu Lys Gly Arg Ser Leu Thr Ser Asp Phe						
	365		370		375	
tgacagctct cagggaaacgg aaatggggag tgcaagacgt caaccaggac aattacatcg						1611
atgcatttga gtgtatggtg tgcaccaagg tgtgggctaa tatcaggctt caggaaaagg						1671
gcttaccacc caaaagatgg gaggcagaag ataccacct gagttgccca gagcccacag						1731
tgtttgcttt ctcaccactc cggactccac ctttgagctc tttgcgagag atgtggattt						1791
ccagctttga acaatccaag aaagaagccc aggcactaag gtggctgggt gataggaatc						1851
aaaacttttc atctcaagag ttttggggcc tagtattcaa ggactgattt caaaaatgat						1911
cagaatgaaa cagaaaaaaa aaaaaaaaaa a						1942

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 seq GVGLVTLLGLAVG/SY

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Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu	
-25 -20 -15	
ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc tac ttg	158
Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu	
-10 -5 1	
gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc aat gaa	206
Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu	
5 10 15	
aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac aac acc	254
Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr	
20 25 30 35	
aag agg ttc cgc ttt gcc ctg ccc acc gcc cac cac act ctg ggg ctg	302
Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu	
40 45 50	
cct gtg ggc aaa cat atc tac ctc tcc acc cga att gat ggc agc ctg	350
Pro Val Gly Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu	
55 60 65	
gtc atc agg cca tac act cct gtc acc agt gat gag gat caa ggc tat	398

Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	Gly	Tyr		
		70					75				80						
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Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe		
	85					90					95						
cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	gtt	ggg	494	
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly		
100					105					110					115		
gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	act	gga	542	
Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	Thr	Gly		
			120						125					130			
aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	gaa	ccc	590	
Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	Glu	Pro		
			135					140					145				
cga	gtg	gag	aag	aaa	ctg	gga	atg	att	gcc	ggc	ggg	aca	gga	atc	acc	638	
Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	Ile	Thr		
		150					155					160					
cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	gat	cca	686	
Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	Asp	Pro		
		165				170					175						
acc	cag	tgc	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	atc	atc	734	
Thr	Gln	Cys	Phe	Leu	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	Ile	Ile		
					185					190					195		
ttg	cgg	gag	gac	tta	gag	gaa	ctg	cag	gcc	cgc	tat	ccc	aat	cgc	ttt	782	
Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	Arg	Phe		
				200					205					210			
aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	tac	agc	830	
Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	Tyr	Ser		
			215				220					225					
aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac	ctg	ccc	gct	cca	878	
Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	Ala	Pro		
		230					235					240					
ggg	gat	gat	gtg	ctg	gta	ctg	ctt	tgt	ggg	cca	ccc	cca	atg	gtg	cag	926	
Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	Val	Gln		
		245				250				255							
ctg	gcc	tgc	cat	ccc	aac	ttg	gac	aaa	ctg	ggc	tac	tca	caa	aag	atg	974	
Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	Lys	Met		
					265				270						275		
cga	ttc	acc	tac	tgagcatcct	ccagcttccc	tggtgctggt	cgctgcagtt									1026	
Arg	Phe	Thr	Tyr														
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ttttcagtta	catctagagc	tgaaatctgg	atagtacctg	caggaacaat	attcctgtag											1146	
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tgtacgcttg	gtccaagatt	ggctagttcc	ttgatagcat	cttactctca	ccttctttgt											1326	
gtctgtgatg	aaaggaacag	tctgtgcaat	gggttttact	taaacttcac	tgttcaacct											1386	
atgagcaaat	ctgtatgtgt	gagtataagt	tgagcatagc	atacttccag	aggtggtctt											1446	
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atcgaaaact	gctgtttgtg	gcaggaaccc	ctggctgtgc	aaataaatgg	ggctgaggcc											1626	
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score 11.6921972463885  
seq LLLCLALSGAAET/KP

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ggcgggtgggc aaggaggggaa ctcgagagca gcctcc atg ggc aca cag gag ggc      174
                               Met Gly Thr Gln Glu Gly
                               -20
tgg tgc ctg ctg ctc tgc ctg gct cta tct gga gca gca gaa acc aag      222
Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys
-15                               -10                               -5                               1
ccc cac cca gca gag ggg cag ttg cgg gca gtg gac gtg gtc cta gac      270
Pro His Pro Ala Glu Gly Gln Leu Arg Ala Val Asp Val Val Leu Asp
                               5                               10                               15
tgc ttc ctg gcg aag gac ggt gcg cac cgt gga gct ctc gcc agc agt      318
Cys Phe Leu Ala Lys Asp Gly Ala His Arg Gly Ala Leu Ala Ser Ser
                               20                               25                               30
gag gac agg gca agg gcc tcc ctt gtg ctg aag cag gtg cca gtg ctg      366
Glu Asp Arg Ala Arg Ala Ser Leu Val Leu Lys Gln Val Pro Val Leu
                               35                               40                               45
gac gat ggc tcc ctg gag gac ttc acc gat ttc caa ggg ggc aca ctg      414
Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp Phe Gln Gly Gly Thr Leu
50                               55                               60                               65
gcc caa gat gac cca cct att atc ttt gag gcc tca gtg gac ctg gtc      462
Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu Ala Ser Val Asp Leu Val
                               70                               75                               80
cag att ccc cag gcc gag gcc ttg ctc cat gct gac tgc agt ggg aag      510
Gln Ile Pro Gln Ala Glu Ala Leu Leu His Ala Asp Cys Ser Gly Lys
                               85                               90                               95
gag gtg acc tgt gag atc tcc cgc tac ttt ctc cag atg aca gag acc      558
Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe Leu Gln Met Thr Glu Thr
100                               105                               110
act gtt aag aca gca gct tgg ttc atg gcc aac atg cag gtc tct gga      606
Thr Val Lys Thr Ala Ala Trp Phe Met Ala Asn Met Gln Val Ser Gly
115                               120                               125
ggg gga cst agc atc tcc ttg gtg atg aag act ccc agg gtc acc aag      654
Gly Gly Xaa Ser Ile Ser Leu Val Met Lys Thr Pro Arg Val Thr Lys
130                               135                               140                               145
aat gag gcg ctc tgg cac ccg acg ctg aac ttg cca ctg agc ccc cag      702
Asn Glu Ala Leu Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln
150                               155                               160
ggg act gtg cga act gca gtg gag ttc cag gtg atg aca cag acc caa      750
Gly Thr Val Arg Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln
165                               170                               175
tcc ctg agc ttc ctg ctg ggg tcc tca gcc tcc ttg gac tgt ggc ttc      798
Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe
180                               185                               190
tcc atg gca ccg ggc ttg gac ctc atc agt gtg gag tgg cga ctg cag      846
Ser Met Ala Pro Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln
195                               200                               205

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His Lys Gly Arg Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly	
210 215 220 225	
cag gct gtg cgg aag ggc gct acc ctg gag cct gca caa ctg ggc atg	942
Gln Ala Val Arg Lys Gly Ala Thr Leu Glu Pro Ala Gln Leu Gly Met	
230 235 240	
gcc agg gat gcc tcc ctc acc ctg ccc ggc ctc act ata cag gac gag	990
Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu	
245 250 255	
ggg acc tac att tgc cag atc acc acc tct ctg tac cga gct cag cag	1038
Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln	
260 265 270	
atc atc cag ctc aac atc caa gct tcc cct aaa gta cga ctg agc ttg	1086
Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu	
275 280 285	
gca aac gaa gct ctg ctg ccc acc ctc atc tgc gac att gct ggc tat	1134
Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr	
290 295 300 305	
tac cct ctg gat gtg gtg gtg acg tgg acc cga gag gag ctg ggt gga	1182
Tyr Pro Leu Asp Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly	
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Ser Pro Ala Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser	
325 330 335	
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Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly	
340 345 350	
tct gca ggt gcc act tac acc tgc cag gtc aca cac atc tct ctg gag	1326
Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val Thr His Ile Ser Leu Glu	
355 360 365	
gag ccc ctt ggg gcc agc acc cag gtt gtc cca cca gag cgg aga aca	1374
Glu Pro Leu Gly Ala Ser Thr Gln Val Val Pro Pro Glu Arg Arg Thr	
370 375 380 385	
gcc ttg gga gtc atc ttt gcc agc agt ctc ttc ctt ctt gca ctg atg	1422
Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met	
390 395 400	
ttc ctg ggg ctt cag aga cgg caa gca cct aca gga ctt ggg ctg ctt	1470
Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu	
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cag gct gaa cgc taggagacca cttcctgtgc tgacacacag agctcccatc	1522
Gln Ala Glu Arg	
420	
tccatgaaga ccgcacagcg cgtgtaagcc agcccagctg acctaaagcg acatgagact	1582
actagaaaga aacgacaccc ttcccccaagc cccacagct actccaaccc aaacaacaac	1642
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<211> 1871

<212> DNA

<213> Homo sapiens

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<222> 195..1052

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<221> sig\_peptide

<222> 195..338

<223> Von Heijne matrix

score 3.50178852790004

seq LGVFFVCHQLSSS/LN

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ttccttagac	aagacacagt	gtagggcccg	gcccgtgttg	gccccaggac	tcctttggaa	180
tatagctgtg	gaca atg aat cct gcg agc gat ggg ggc aca tca gag agc	230				
	Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser					
	-45	-40				
att ttt gac ctg gac tat gca tcc tgg ggg atc cgc tcc acg ctg atg	278					
Ile Phe Asp Leu Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met						
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gtc gct ggc ttt gtc ttc tac ttg ggc gtc ttt gtg gtc tgc cac cag	326					
Val Ala Gly Phe Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln						
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ctg tcc tct tcc ctg aat gcc act tac cgt tct ttg gtg gcc aga gag	374					
Leu Ser Ser Ser Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu						
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aag gtc ttc tgg gac ctg gcg gcc acg cgt gca gtc ttt ggt gtt cag	422					
Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln						
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agc aca gcc gca ggc ctg tgg gct ctg ctg ggg gac cct gtg ctg cat	470					
Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His						
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gcc gac aag gcg cgt ggc cag cag aac tgg tgc ttt cac atc acg	518					
Ala Asp Lys Ala Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr						
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Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser						
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aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc	614					
Asn Leu Ile Phe Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu						
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ttt gcc ttt ctt ggg ttt ctt ggc tgc ttg gtc aat ctc caa gct ggc	662					
Phe Ala Phe Leu Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly						
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cac tat cta gct atg acc acg ttg ctc ctg gag atg agc acg ccc ttt	710					
His Tyr Leu Ala Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe						
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acc tgc gtt tcc tgg atg ctc tta aag gcg ggc tgg tcc gag tct ctg	758					
Thr Cys Val Ser Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu						
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Phe Trp Lys Leu Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg						
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atg gtt cta acc tac cac atg tgg tgg gtg tgt ttc tgg cac tgg gac	854					
Met Val Leu Thr Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp						
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ggc ctg gtc agc agc ctg tat ctg cct cat ttg aca ctg ttc ctt gtc	902					
Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val						
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gga ctg gct ctg ctt acg cta atc att aat cca tat tgg acc cat aag	950					
Gly Leu Ala Leu Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys						
	190	195	200			
aag act cag cag ctt ctc aat ccg gtg gac tgg aac ttc gca cag cca	998					

Lys Thr Gln Gln Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro  
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 Glu Ala Lys Ser Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys  
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 Arg Pro  
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 ggctgaacc tggggccaga caccctctc ccggcc atg gtc aac gac cct cca 234  
 Met Val Asn Asp Pro Pro  
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 Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly  
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 Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr  
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 Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr  
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 agg acc gac tgt gat tcc tcc acc acc tca ctc tgc tcc ttc cct gtt 474  
 Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser Leu Cys Ser Phe Pro Val

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Ala Asn Val Ser Leu Thr Lys Gly Gly Arg Asp Arg Val Leu Met Tyr								
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gga cag ccg tat cgt gtt acc tta gag ctt gag ctg cca gag tcc cct								570
Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu Glu Leu Pro Glu Ser Pro								
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gtg aat caa gat ttg ggc atg ttc ttg gtc acc att tcc tgc tac acc								618
Val Asn Gln Asp Leu Gly Met Phe Leu Val Thr Ile Ser Cys Tyr Thr								
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aga ggt ggc cga atc atc tcc act tct tcg cgt tcg gtg atg ctg cat								666
Arg Gly Arg Ile Ile Ser Thr Ser Ser Arg Ser Val Met Leu His								
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tac cgc tca gac ctg ctc cag atg ctg gac aca ctg gtc ttc tct agc								714
Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp Thr Leu Val Phe Ser Ser								
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ctc ctg cta ttt ggc ttt gca gag cag aag cag ctg ctg gag gtg gaa								762
Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys Gln Leu Leu Glu Val Glu								
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ctc tac gca gac tat aga gag aac tcg tac gtg ccg acc act gga gcg								810
Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr Val Pro Thr Thr Gly Ala								
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atc att gag atc cac agc aag cgc atc cag ctg tat gga gcc tac ctc								858
Ile Ile Glu Ile His Ser Lys Arg Ile Gln Leu Tyr Gly Ala Tyr Leu								
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cgc atc cac gcg cac ttc act ggg ctc aga tac ctg cta tac aac ttc								906
Arg Ile His Ala His Phe Thr Gly Leu Arg Tyr Leu Leu Tyr Asn Phe								
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ccg atg acc tgc gcc ttc ata ggt gtt gcc agc aac ttc acc ttc ctc								954
Pro Met Thr Cys Ala Phe Ile Gly Val Ala Ser Asn Phe Thr Phe Leu								
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Ser Val Ile Val Leu Phe Ser Tyr Met Gln Trp Val Trp Gly Gly Ile								
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tgg ccc cga cac cgc ttc tct ttg cag gtt aac atc cga aaa aga gac								1050
Trp Pro Arg His Arg Phe Ser Leu Gln Val Asn Ile Arg Lys Arg Asp								
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aat tcc cgg aag gaa gtc caa cga agg atc tct gct cat cag cca ggg								1098
Asn Ser Arg Lys Glu Val Gln Arg Arg Ile Ser Ala His Gln Pro Gly								
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cct gaa ggc cag gag gag tca act ccg caa tca gat gtt aca gag gat								1146
Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp								
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ggt gag agc cct gaa gat ccc tca ggg aca gag ggt cag ctg tcc gag								1194
Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu								
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gag gag aaa cca gat cag cag ccc ctg agc gga gag gag cta gag								1242
Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu								
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cct gag gcc agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg								1290
Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu								
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acg gag gcc aac ctg cct gct cct gct cct gct tct gct tct gcc cct								1338
Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro								
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gtc cta gag act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga								1386
Val Leu Glu Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg								
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 Gln Arg Pro Thr Cys Ser Ser  
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 gcttcgaaaa aaaaaaaaaa aaa 1523

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 Met Arg Gln Lys  
 -20  
 gcg gta tcg ctt ttc ttc tgc tac ctg ctg ctc ttc act tgc agt ggg 162  
 Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly  
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 Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala  
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 Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala  
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 Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly  
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 Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly  
 65 70 75 80  
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 Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly  
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 Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu  
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 ccaggctaga gtgcagtggc tattcacaga tgcgaacata gtacactgca gcctccaact 672  
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 tcgcttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180  
 agtgctcgga gagctcggac agcgggtccg ggttctggaa ggccctgacc ttc atg 236  
 Met  
 -20  
 gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284  
 Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe  
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 Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser  
 1 5 10  
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 Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val  
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 Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly  
 30 35 40 45  
 aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476  
 Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser  
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 Glu Glu Asp Glu Glu  
 65  
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 <222> 180..800

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<222> 180..248

<223> Von Heijne matrix

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tcaggccctg ccgccatcgc cgcagatcca gcgcccagag agacaccaga gaaccacc 179
atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg 227
Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
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Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
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Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10 15 20 25
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Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
30 35 40
atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac 419
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
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Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
60 65 70
cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg 515
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
75 80 85
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Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90 95 100 105
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Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
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Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
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Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
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Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
155 160 165
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Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170 175 180
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<222> 140..211

<223> Von Heijne matrix

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aagtgggtcta taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca      172
                               Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser
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ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta      220
Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val
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gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg      268
Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala
                               5                               10                               15

ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa      316
Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys
20                               25                               30                               35

tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg      364
Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp
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att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc      412
Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala
                               55                               60                               65

ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg      460
Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val
70                               75                               80

aga ttt aac att tagaggtgac agcatccccc acactggcag ttaatttttt      512
Arg Phe Asn Ile
85

gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat      572
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<212> DNA

<213> Homo sapiens

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<221> sig\_peptide

<222> 68..112

<223> Von Heijne matrix

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<400> 52

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1 5 10 15		
gaa tgt gat tac att aat gct aga tca tgt tgc tca aaa tta aac aag		205
Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys		
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Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu		
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Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala		
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Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly		
65 70 75		
gtg ttt gat cca aca gaa ata cac aat cga ggg cag ctg aag tca cac		397
Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His		
80 85 90 95		
atg aaa gaa gcc atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc		445
Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe		
100 105 110		
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Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp		
115 120		
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Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser		
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Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn		

	15		20		25		
act tta gaa gaa ctg gaa gtg gtc tgc gaa agt tgt gtg gaa gtt cag							247
Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln							
	30		35		40		
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca							295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr							
	45		50		55		
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta							343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val							
	60		65		70		75
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att							391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile							
	80		85		90		
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat							439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn							
	95		100		105		
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa							487
Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu							
	110		115		120		
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt ttttaagagcc							537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp							
	125		130				
actggcctgt aattgtttga tatatttgta actctttgta taatgtcaga gactcatggt							597
taatacatag gtgatttgta cctcagagca ttttttaaag gattctttcc aagcgagatt							657
taattataag gtagtaccta atttggttcaa tgtataacat tctcaggatt tgtaacactt							717
aaatgatcag acagaataat attttctagt tattatgtgt aagatgagtt gctatttttc							777
tgatgctcat tctgatacaa ctatttttcg tgtcaaatat ctactgtgcc caaatgtact							837
caatttaaat cattactctg taaaataaat aagcagatga ttcttataaa aaaaaaaaaa							897

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 <222> 92..634

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 score 7.36306712986597  
 seq FLLLTCLFITGTS/VS

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ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc	112
Met Pro Pro Phe Leu Leu Leu	
-15 -10	
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat	160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp	
-5 1 5	
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac	208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp	
10 15 20	
cac cag ttg gat gag tct caa ggt cct cct cta tgt gac aac cat gtg	256
His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys Asp Asn His Val	

25	30	35	
aat ggg gag tgg tac cac ttc acg ggc atg gcg gga gat gcc atg cct			304
Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly Asp Ala Met Pro			
40	45	50	55
acc ttc tgc ata cca gaa aac cac tgt gga acc cac gca cct gtc tgg			352
Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp			
60	65	70	
ctc aat ggc agc cac ccc cta gaa ggc gac ggc att gtg caa cgc cag			400
Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln			
75	80	85	
gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg aac acc acg gtg			448
Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val			
90	95	100	
gaa gtc aag gct tgc cct gga ggc tac tat gtg tat cgt ctg acc aag			496
Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys			
105	110	115	
ccc agc gtc tgc ttc cac gtc tac tgt ggt cgt gag tac ctt ccc tgt			544
Pro Ser Val Cys Phe His Val Tyr Cys Gly Arg Glu Tyr Leu Pro Cys			
120	125	130	135
gct ctt ttt ctc cac caa caa ggc cac agg tgg agt cca aaa gtg ccc			592
Ala Leu Phe Leu His Gln Gln Gly His Arg Trp Ser Pro Lys Val Pro			
140	145	150	
aat tat agg ata tgc agt tac agt ggc aac tat atc tca atc			634
Asn Tyr Arg Ile Cys Ser Tyr Ser Gly Asn Tyr Ile Ser Ile			
155	160	165	
tgaacaacat tgatgtgggg ctaaagatac tctgatttct gagatctctt cttagaactt			694
ctgaaaaatt cctgaagaaa tagaagggga aaggagctat gactttgatc agttcttttt			754
aattttgtct gaattccatt caaacaaaac attagaaaat gaaacattgg gccaggcgca			814
gtggctcatg cctgtaatcc cagcactttg ggaggctgag gcgggtggat cacaagatca			874
ggagtttaag accagcctgg ccaatatggt gaaacctgt ctctactaga aatacaaaaa			934
ttagacaggc gtggtggcag gcaactgtaa cccagctac ccgggaggct gaggcaggag			994
aattgcttga acccgggagg tggacgttgc ggtcaggcga aaatcgtgcc attgcactcc			1054
agcctgggtg acagagttag actctgattc aaaaaaaaaa aaaaaaaa			1101

<210> 55  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 27..767

<220>  
 <221> sig\_peptide  
 <222> 27..80  
 <223> Von Heijne matrix  
 score 8.96664802487992  
 seq LFCLAVLAASSFS/KA

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agcagaggcc ctacacccac cgaggc atg ggg ctc cct ggg ctg ttc tgc ttg	53
Met Gly Leu Pro Gly Leu Phe Cys Leu	
-15	-10
gcc gtg ctg gct gcc agc agc ttc tcc aag gca cgg gag gaa gaa att	101
Ala Val Leu Ala Ala Ser Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile	
-5	1
acc cct gtg gtc tcc att gcc tac aaa gtc ctg gaa gtt ttc ccc aaa	149

Thr	Pro	Val	Val	Ser	Ile	Ala	Tyr	Lys	Val	Leu	Glu	Val	Phe	Pro	Lys	
	10						15					20				
ggc	cgc	tgg	gtg	ctc	ata	acc	tgc	tgt	gca	ccc	cag	cca	cca	ccg	ccc	197
Gly	Arg	Trp	Val	Leu	Ile	Thr	Cys	Cys	Ala	Pro	Gln	Pro	Pro	Pro	Pro	
	25						30				35					
atc	acc	tat	tcc	ctc	tgt	gga	acc	aag	aac	atc	aag	gtg	gcc	aag	aag	245
Ile	Thr	Tyr	Ser	Leu	Cys	Gly	Thr	Lys	Asn	Ile	Lys	Val	Ala	Lys	Lys	
	40					45				50					55	
gtg	gtg	aag	acc	cac	gag	ccg	gcc	tcc	ttc	aac	ctc	aac	gtc	aca	ctc	293
Val	Val	Lys	Thr	His	Glu	Pro	Ala	Ser	Phe	Asn	Leu	Asn	Val	Thr	Leu	
				60					65					70		
aag	tcc	agt	cca	gac	ctg	ctc	acc	tac	ttc	tgc	cgg	gcg	tcc	tcc	acc	341
Lys	Ser	Ser	Pro	Asp	Leu	Leu	Thr	Tyr	Phe	Cys	Arg	Ala	Ser	Ser	Thr	
			75					80					85			
tca	ggg	gcc	cat	gtg	gac	agt	gcc	agg	cta	cag	atg	cac	tgg	gag	ctg	389
Ser	Gly	Ala	His	Val	Asp	Ser	Ala	Arg	Leu	Gln	Met	His	Trp	Glu	Leu	
	90						95					100				
tgg	tcc	aag	cca	gtg	tct	gag	ctg	cgg	gcc	aac	ttc	act	ctg	cag	gac	437
Trp	Ser	Lys	Pro	Val	Ser	Glu	Leu	Arg	Ala	Asn	Phe	Thr	Leu	Gln	Asp	
	105					110					115					
aga	ggg	gca	ggc	ccc	agg	gtg	gag	atg	atc	tgc	cag	gcg	tcc	tcg	ggc	485
Arg	Gly	Ala	Gly	Pro	Arg	Val	Glu	Met	Ile	Cys	Gln	Ala	Ser	Ser	Gly	
	120					125				130					135	
agc	cca	cct	atc	acc	aac	agc	ctg	atc	ggg	aag	gat	ggg	cag	gtc	cac	533
Ser	Pro	Pro	Ile	Thr	Asn	Ser	Leu	Ile	Gly	Lys	Asp	Gly	Gln	Val	His	
					140				145					150		
ctg	cag	cag	aga	cca	tgc	cac	agg	cag	cct	gcc	aac	ttc	tcc	ttc	ctg	581
Leu	Gln	Gln	Arg	Pro	Cys	His	Arg	Gln	Pro	Ala	Asn	Phe	Ser	Phe	Leu	
			155					160				165				
ccg	agc	cag	aca	tcg	gac	tgg	ttc	tgg	tgc	cag	gct	gca	aac	aac	gcc	629
Pro	Ser	Gln	Thr	Ser	Asp	Trp	Phe	Trp	Cys	Gln	Ala	Ala	Asn	Asn	Ala	
			170				175					180				
aat	gtc	cag	cac	agc	gcc	ctc	aca	gtg	gtg	ccc	cca	gga	ggg	ttg	ccc	677
Asn	Val	Gln	His	Ser	Ala	Leu	Thr	Val	Val	Pro	Pro	Gly	Gly	Leu	Pro	
	185					190				195						
agg	gca	ccc	acc	atc	gtg	ctg	gtt	ggc	agc	ctt	gcc	tcc	act	gcg	gcc	725
Arg	Ala	Pro	Thr	Ile	Val	Leu	Val	Gly	Ser	Leu	Ala	Ser	Thr	Ala	Ala	
	200				205					210					215	
atc	acc	tcc	agg	atg	ctg	ggc	tgg	acc	acg	tgg	gcc	agg	tgg			767
Ile	Thr	Ser	Arg	Met	Leu	Gly	Trp	Thr	Thr	Trp	Ala	Arg	Trp			
				220						225						
tgaccagaag	atggaggact	ggcagggtcc	cctggagagc	cccattccttg	ccttgccgct											827
ctacaggagc	accgcgcgtc	tgagtgaaga	ggagtttggg	gggttcagga	tagggaatgg											887
ggaggtcaga	ggacgcaaag	cagcagccat	gtagaatgaa	ccgtccagag	agccaagcac											947
ggcagaggac	tgcaggccat	cagcgtgcac	tgttcgtatt	tggagttcat	gcaaaatgag											1007
tgtgttttag	ctgctcttgc	cacaaaaaaaa	aaaaaaaaaaa													1047

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 <222> 4..399

<220>  
 <221> sig\_peptide

<222> 4..126  
 <223> Von Heijne matrix  
 score 4.34454795165846  
 seq RVVSWLFSIVVFG/SI

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 acg atg gaa ggg ggt gcg tac gga gcg ggc aaa gcc ggg ggc gcc ttc 48  
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe  
 -40 -35 -30  
 gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg 96  
 Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val  
 -25 -20 -15  
 tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc 144  
 Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly  
 -10 -5 1 5  
 tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc 192  
 Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg  
 10 15 20  
 aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc 240  
 Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe  
 25 30 35  
 ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc 288  
 Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile  
 40 45 50  
 agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc 336  
 Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val  
 55 60 65 70  
 tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag 384  
 Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu  
 75 80 85  
 ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg tttcagatga 439  
 Gly Cys Pro Gly Pro  
 90  
 gggaaatgag ccttctgggc tttcctctgg ttcgtgggat tctgctacct ggccaaccag 499  
 tggcaggtct ccaagcccaa ggacaacca ctgaacgaag ggacggacgc agcccgggcc 559  
 gccatgcct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggccgtg 619  
 cggagattca aggacctaag cttccaggag gactacagca cactgttccc tgcttcggca 679  
 cagccgtagg cctccccggc ttgcagaggc cggcagccct gtatcaccct tggcagttag 739  
 gtggcaggag cagcctagtg ccagaaatgt ccaagatgcc agggcatgca gggcagtgga 799  
 aggtggctt gaggaaccaa ttcagggtct ccactgactc attcattcct tcaccgcctc 859  
 cttcattgat tcttcattgag ttcattcatt cagtaaacad ttattgagta aaaaaaaaaa 919  
 aaaaaa 925

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 127..879

<220>  
 <221> sig\_peptide  
 <222> 127..198  
 <223> Von Heijne matrix  
 score 5.38660866264012  
 seq ALCSVCSMSVLRA/YP

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gccaggagag tcccagacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag      120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
      -20      -15
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
-10      -5      1      5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
      10      15      20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
      25      30      35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
      40      45      50
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
      55      60      65      70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
      75      80      85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
      90      95      100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
      105      110      115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
      120      125      130
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
      135      140      145      150
cgg cgg cac acc cgg agc gcc gag gac gac tgc gag cgg gac ccc ctg      696
Arg Arg His Thr Ser Ala Glu Asp Ser Glu Arg Asp Pro Leu
      155      160      165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170      175      180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185      190      195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
      200      205      210
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      215      220      225
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggtc      949
ccttgacgtt ccgaggatgg gaaagggtgac agggggcatgt atggaatttg ctgcttctct      1009
gggggtccctt ccacaggagg tctgtgaga accaaccttt gagggccaaag tcatgggggtt      1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa      1129
ctagaaattt ccccttcctg aaggtagaga gaaggggtct ctcccaacat atttctcttc      1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa a      1240

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 156..566

<220>  
 <221> sig\_peptide  
 <222> 156..221  
 <223> Von Heijne matrix  
 score 5.67458379966095  
 seq LVSMAGRVCLCQG/SA

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cctcactcct ggcgtctgag tctctggcgt agccc atg ctg agt ggg cgg ctg      173
                               Met Leu Ser Gly Arg Leu
                               -20
gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc      221
Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly
-15 -10 -5
agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg      269
Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr
1 5 10 15
aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag      317
Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu
20 25 30
agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg      365
Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val
35 40 45
gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac      413
Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His
50 55 60
cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat      461
Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His
65 70 75 80
gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct      509
Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser
85 90 95
cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta      557
Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu
100 105 110
gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg      606
Gly Thr Pro
115
ggtgagcacg aattaccgag gccttccctt tgatacagtc caggatttgt aagggatgaa      666
gacccctggg cccattctg ttgggggtcca tacatactct ccgaagatag caacttgctt      726
caggtcaaag tgaacccgag aaaagagaag aatcactcac tactgctctt gccctggact      786
attcaggaag ggcagcccgg atgttccatg ttaaatcgtg acagaattgc accagacctg      846
atgagttgga aacaatccta tacattaaaa gaaattacac taaaaaaaaa aaaaaa      902

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<210> 59  
 <211> 1969

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 35..1657

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<221> sig\_peptide  
<222> 35..118  
<223> Von Heijne matrix  
score 3.75144398608723  
seq SGLLLQVLFRLIT/FV

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Met Gly Ser Gln Glu Val Leu  
-25  
ggc cac gcg gcc cgg ctg gcc tcc tcc ggt ctc ctc ctg cag gtg ttg 103  
Gly His Ala Ala Arg Leu Ala Ser Ser Gly Leu Leu Leu Gln Val Leu  
-20 -15 -10  
ttt cgg ttg atc acc ttt gtc ttg aat gca ttt att ctt cgc ttc ctg 151  
Phe Arg Leu Ile Thr Phe Val Leu Asn Ala Phe Ile Leu Arg Phe Leu  
-5 1 5 10  
tca aag gaa atc gtt ggc gta gta aat gta aga cta acg ctg ctt tac 199  
Ser Lys Glu Ile Val Gly Val Val Asn Val Arg Leu Thr Leu Leu Tyr  
15 20 25  
tca acc acc ctc ttc ctg gcc aga gag gcc ttc cgc aga gca tgt ctc 247  
Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala Phe Arg Arg Ala Cys Leu  
30 35 40  
agt ggg ggc acc cag cga gac tgg agc cag acc ctc aac ctg ctg tgg 295  
Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln Thr Leu Asn Leu Leu Trp  
45 50 55  
cta aca gtc ccc ctg ggt gtg ttt tgg tcc tta ttc ctg ggc tgg atc 343  
Leu Thr Val Pro Leu Gly Val Phe Trp Ser Leu Phe Leu Gly Trp Ile  
60 65 70 75  
tgg ttg cag ctg ctt gaa gtg cct gat cct aat gtt gtc cct cac tat 391  
Trp Leu Gln Leu Leu Glu Val Pro Asp Pro Asn Val Val Pro His Tyr  
80 85 90  
gca act gga gtg gtg ctg ttt ggt ctc tcg gca gtg gtg gag ctt cta 439  
Ala Thr Gly Val Val Leu Phe Gly Leu Ser Ala Val Val Glu Leu Leu  
95 100 105  
gga gag ccc ttt tgg gtc ttg gca caa gca cat atg ttt gtg aag ctc 487  
Gly Glu Pro Phe Trp Val Leu Ala Gln Ala His Met Phe Val Lys Leu  
110 115 120  
aag gtg att gca gag agc ctg tcg gta att ctt aag agc gtt ctg aca 535  
Lys Val Ile Ala Glu Ser Leu Ser Val Ile Leu Lys Ser Val Leu Thr  
125 130 135  
gct ttt ctc gtg ctg tgg ttg cct cac tgg gga ttg tac att ttc tct 583  
Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser  
140 145 150 155  
ttg gcc cag ctt ttc tat acc aca gtt ctg gtg ctc tgc tat gtt att 631  
Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile  
160 165 170  
tat ttc aca aag tta ctg ggt tcc cca gaa tca acc aag ctt caa act 679  
Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu Ser Thr Lys Leu Gln Thr  
175 180 185  
ctt cct gtc tcc aga ata aca gat ctg tta ccc aat att aca aga aat 727

Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	Pro	Asn	Ile	Thr	Arg	Asn	
	190						195					200				
gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	ctg	act	tgg	agt	ttt	ttc	775
Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	Leu	Thr	Trp	Ser	Phe	Phe	
	205					210					215					
aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	gaa	ggc	gag	cga	tat	gtg	823
Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	Glu	Gly	Glu	Arg	Tyr	Val	
220					225					230					235	
atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	ggt	gat	cag	ggg	gtg	tat	gat	871
Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	Asp	Gln	Gly	Val	Tyr	Asp	
				240					245					250		
ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	aga	tta	att	ttc	cag	cca	919
Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	Ala	Arg	Leu	Ile	Phe	Gln	Pro	
				255				260					265			
ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	gct	aag	gtg	ctg	gag	agg	gga	967
Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	Lys	Val	Leu	Glu	Arg	Gly	
	270						275					280				
aag	gat	gcc	aca	ctt	cag	aag	cag	gag	gac	gtt	gct	gtg	gct	gct	gca	1015
Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	Val	Ala	Val	Ala	Ala	Ala	
	285					290					295					
gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	ctg	ctg	gcc	ggc	ctg	acc	atc	1063
Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	Leu	Ala	Gly	Leu	Thr	Ile	
300					305					310					315	
act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	gct	ctg	gat	atc	tac	gga	1111
Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	Ala	Leu	Asp	Ile	Tyr	Gly	
				320				325						330		
ggg	acc	atg	ctt	agc	tca	gga	tcc	ggt	cct	gtt	ttg	ctg	cgt	tcc	tac	1159
Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	Val	Leu	Leu	Arg	Ser	Tyr	
			335					340					345			
tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	aat	gga	gtg	aca	gag	tgt	tta	1207
Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	Gly	Val	Thr	Glu	Cys	Leu	
	350						355					360				
aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	gtc	gac	agg	tac	aat	ttt	gtg	1255
Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val	Asp	Arg	Tyr	Asn	Phe	Val	
	365					370					375					
atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	gtg	tta	tcc	tat	ctc	ttg	acc	1303
Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val	Leu	Ser	Tyr	Leu	Leu	Thr	
380					385					390					395	
cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	ttg	gcc	aac	tgc	ttt	aac	atg	1351
Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu	Ala	Asn	Cys	Phe	Asn	Met	
				400				405						410		
ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	atc	cac	cgc	tac	tac	cga	1399
Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe	Ile	His	Arg	Tyr	Tyr	Arg	
			415					420					425			
agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	cac	cta	tcg	cca	gtc	ctg	1447
Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu	His	Leu	Ser	Pro	Val	Leu	
		430					435					440				
ctc	ggg	aca	ttt	gcc	ctc	agt	ggt	ggg	gtt	act	gct	gtt	tcg	gag	gta	1495
Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val	Thr	Ala	Val	Ser	Glu	Val	
	445					450					455					
ttc	ctc	tgc	tgt	gat	cag	ggc	tgg	cca	gcc	aga	ctg	gca	cac	att	gct	1543
Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro	Ala	Arg	Leu	Ala	His	Ile	Ala	
460					465					470					475	
gtg	ggg	gcc	ttc	tgt	ctg	gga	gca	act	ctc	ggg	aca	gca	ttc	ctc	aca	1591
Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	Gly	Thr	Ala	Phe	Leu	Thr	
				480					485					490		
gag	acc	aag	ctg	atc	cat	ttc	ctc	agg	act	cag	tta	ggt	gtg	ccc	aga	1639
Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	Thr	Gln	Leu	Gly	Val	Pro	Arg	

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          495          500          505
cgc act gac aaa atg aca tgacttcagg gaagcctgga caccgcaggc 1687
Arg Thr Asp Lys Met Thr
      510
acctggacca gctatgggta gttctgtggg tggaacacat tctgtgtaag agccccactg 1747
agggctctgc agcggagtga cagcaacccc agagatgagg caccagagag tgccactgca 1807
tgagacacct gtgaccattc gaagtctgaa atgcgggggg ggagtttcat ttttaagtga 1867
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<210> 60
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 77..937

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<220>
<221> sig_peptide
<222> 77..127
<223> Von Heijne matrix
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      seq RIVSAALLAFVQT/HL

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gagcagaaga gagagc atg gag ctg gag agg atc gtc agt gca gcc ctc ctt 112
      Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
          -15          -10
gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat 160
Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
-5          1          5          10
gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc 208
Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
      15          20          25
tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag atg 256
Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
      30          35          40
atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata 304
Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
      45          50          55
ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac 352
Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
      60          65          70          75
aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc 400
Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
      80          85          90
atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act 448
Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
      95          100          105
agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc 496
Arg Ser Ser Ala Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
      110          115          120
gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg ttc 544
Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe
      125          130          135

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cct acc tgt tgc gtg gag cag gcc cag tgg gtg ctg gcc aaa gct cgg      592
Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg
140                               145                               155
ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa gag      640
Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu
                               160                               165                               170
ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc ctc      688
Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu
                               175                               180                               185
aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag tac      736
Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
190                               195                               200
atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
205                               210                               215
ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag gta      832
Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val
220                               225                               230                               235
gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag gcc      880
Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala
240                               245                               250
gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag tac      928
Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr
255                               260                               265
cgc ttc cat tgaggcactc gccggactct gcccgagcct tctaggctca      977
Arg Phe His
270
gatcccagag ggatgcagga gccctatacc cctacacagg ggccccctaa ctctgtccc      1037
ccttctctac tcctttgtct catagtgtta acctactctc ggagctgcct ccatgggcac      1097
agtaaagggtg gcccaaggaa aaaaaaaaaa aaaaa      1132

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<210> 61  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 9..503

<220>  
 <221> sig\_peptide  
 <222> 9..113  
 <223> Von Heijne matrix  
 score 10.2506494380376  
 seq LLPLVLLPPLAAA/AA

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<400> 61
tgccaggg atg atg cgc tgc tgc cgc cgc cgc tgc tgc tgc cgg caa cca      50
Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro
-35                               -30                               -25
ccc cat gcc ctg agg ccg ttg ctg ttg ctg ccc ctc gtc ctt tta cct      98
Pro His Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro
-20                               -15                               -10
ccc ctg gca gca gct gca gcg ggc cca aac cga tgt gac acc ata tac      146
Pro Leu Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr
-5                               1                               5                               10
cag ggc ttc gcc gag tgt ctc atc cgc ttg ggg gac agc atg ggc cgc      194

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Gln Gly Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg	
15 20 25	
gga ggc gag ctg gag acc atc tgc agg tct tgg aat tac ttc cat gcc	242
Gly Gly Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala	
30 35 40	
tgt gcc tct cag gtc ctg tca ggc tgt ccg gag gag gca gct gca gtg	290
Cys Ala Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val	
45 50 55	
tgg gaa tca cta cag caa gaa gct cgc cag gcc ccc cgt ccg aat aac	338
Trp Glu Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn	
60 65 70 75	
ttg cac act ctg tgc ggt gcc ccg gtg cat gtt cgg gag cgc ggc aca	386
Leu His Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr	
80 85 90	
ggc tcc gaa acc aac cag gag acg ctg cgg gct aca gcg cct gca ctc	434
Gly Ser Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu	
95 100 105	
ccc atg gcc cct gcg ccc cca ctg ctg gcg gct gct ctg gct ctg gcc	482
Pro Met Ala Pro Ala Pro Pro Leu Leu Ala Ala Leu Ala Leu Ala	
110 115 120	
tac ctc ctg agg cct ctg gcc tagcttggtg ggttggttag cagcgcccg	533
Tyr Leu Leu Arg Pro Leu Ala	
125 130	
acctccagcc ctgctctggc ggttggttgtc caggctctgc agagcgcagc agggcttttc	593
attaaaggta tttatatttg caaaaaaaaa aaaaaaaaa	631

<210> 62  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 21..464

<220>  
 <221> sig\_peptide  
 <222> 21..95  
 <223> Von Heijne matrix  
 score 5.38058532480537  
 seq AVTSLLSPTPATA/LA

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ggaagtgagt gatcgaaagc atg gcg tgc gtg gtg ttg gcg ctg agg acc cgg	53
Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg	
-25 -20 -15	
aca gcc gtt aca tcc ttg cta agc ccc act ccg gct aca gct ctt gct	101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala	
-10 -5 1	
gtc aga tac gca tcc aag aag tgc ggt ggt agc tcc aaa aac ctc ggt	149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly	
5 10 15	
gga aag tca tca ggc aga cgc caa ggc att aag aaa atg gaa ggt cac	197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His	
20 25 30	
tat gtt cat gct ggg aac atc att gca aca cag cgc cat ttc cgc tgg	245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp	
35 40 45 50	

cac cca ggt gcc cat gtg ggt gtt ggg aag aat aaa tgt ctg tat gcc	293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala	
55 60 65	
ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat	341
Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His	
70 75 80	
ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt	389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly	
85 90 95	
gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag	437
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu	
100 105 110	
ggc acc ttc aaa ctg gta gct atg ctt tgaatgtcctg ttgaggccat	484
Gly Thr Phe Lys Leu Val Ala Met Leu	
115 120	
cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca agggttgggg	544
tggcgacacg gcctcccag gaagaggtct gcttgatggt gactctgcag gagactctga	604
agtgactgct gggaaaccct ttgggagacc tgacctgggg ccaaaaaataa agtgagccag	664
cgatcatgaac gcatgctatt tagggacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	722

<210> 63  
 <211> 1442  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 178..1050

<220>  
 <221> sig\_peptide  
 <222> 178..279  
 <223> Von Heijne matrix  
 score 10.0571391689271  
 seq FLCLLSALLLLEGG/KK

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gcagagatac agaggcagag gaaaagggca ctcctatgtg acctgttctt agagcaagac	120
aatcaccatc tgaattccag aagccctgtt catggttggg gatattttct cgactgc	177
atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg	225
Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu	
-30 -25 -20	
aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act	273
Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Thr	
-15 -10 -5	
gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt	321
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys	
1 5 10	
acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc	369
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr	
15 20 25 30	
gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act	417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr	
35 40 45	
gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg	465
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu	
50 55 60	



<223> Von Heijne matrix  
score 4.30837886795471  
seq LMVELLKVFVVEA/AV

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Met Glu Gly Ala Gly Ala Gly  
-45  
tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc 100  
Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe  
-40 -35 -30  
aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg 148  
Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val  
-25 -20 -15  
gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg 196  
Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg  
-10 -5 1 5  
cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag 244  
Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu  
10 15 20  
aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct 294  
Lys Val Leu Pro Gln Leu Leu Asp Phe  
25 30  
gaggccaccc ccagaggagc ccttgggtcca cagaagcagg ccttgtgttt ccagcggcct 354  
ctgataagag gcaggggaagg acctgaagga tttggagttg attcaaaciaa gatctctggg 414  
agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca 474  
gtggggacac tgggtgtggga aggggcagca cctggggagt ccttgcctct cctccctggg 534  
acaatagtgt gcatgccacc cgggggtccta caggcagggtg ctgggaaagg cctggccagc 594  
aggtagcctg tgtgtttgac aaacagcagc tggcagcgct gcctcctgcc cacattcctg 654  
ccacccgaca tcaaagctgg cgtgtgacct ttccagccat gcgatattcc ccttgggaaga 714  
tgcttcccc ggctataaat ttgttctcac aaagcaacat caataaatca aaactgtctc 774  
tctcaaaaaa aaaaaaaaaa a 795

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<211> 1236  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 222..920

<220>  
<221> sig\_peptide  
<222> 222..311  
<223> Von Heijne matrix  
score 4.35083245061594  
seq VAHALSLPAESYG/ND

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agtactccac ctctgcgcct gtgcggggag ggtaaggcgg ggccagcaac ttcctcagct 120  
ggagggagag cgcacgggtg agccgccagt tgagaaggac tctgatccgg ctcagctttc 180  
caatcagctg cggaaggagc cacgctttcg ggggttgcaa g atg gcg gcc acc agt 236  
Met Ala Ala Thr Ser  
-30  
gga act gat gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg 284  
Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala

-25	-20	-15	-10	
ctt tct ctc cca gca gag tcg tat ggc aac gat cct gac att gag atg				332
Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp Pro Asp Ile Glu Met				
	-5	1	5	
gct tgg gcc atg aga gca atg cag cat gct gaa gtc tat tac aag ctg				380
Ala Trp Ala Met Arg Ala Met Gln His Ala Glu Val Tyr Tyr Lys Leu				
	10	15	20	
att tca tca gtt gac cca cag ttc ctc aaa ctc acc aaa gta gat gac				428
Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp				
	25	30	35	
caa att tac tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat				476
Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp				
	40	45	50	55
gtg ttg gac cca gaa gaa ctc aag tca gaa tca gcc aaa gag aag tgg				524
Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser Ala Lys Glu Lys Trp				
	60	65	70	
agg cca ttc tgc ttg aag ttt aat ggg att gtt gaa gac ttc aac tat				572
Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val Glu Asp Phe Asn Tyr				
	75	80	85	
ggt act ttg ctg cga cta gat tgt tct cag ggc tac act gag gaa aac				620
Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly Thr Glu Glu Asn				
	90	95	100	
acc atc ttt gcc ccc agg ata caa ttc ttt gcc att gaa att gct cgg				668
Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala Ile Glu Ile Ala Arg				
	105	110	115	
aac cgg gaa ggc tat aac aaa gct gtt tat atc agt gtt cag gac aaa				716
Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile Ser Val Gln Asp Lys				
	120	125	130	135
gaa gga gag aaa gga gtc aac aat gga gga gaa aaa aga gct gac agt				764
Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu Lys Arg Ala Asp Ser				
	140	145	150	
gga gaa gaa gag aac acc aag aat gga gga gag aaa gga gct gat agt				812
Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu Lys Gly Ala Asp Ser				
	155	160	165	
gga gaa gaa aaa gag gaa gga atc aac aga gaa gac aaa act gac aaa				860
Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu Asp Lys Thr Asp Lys				
	170	175	180	
gga gga gaa aaa ggg aaa gaa gct gac aaa gaa atc aac aaa agt ggt				908
Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu Ile Asn Lys Ser Gly				
	185	190	195	
gaa aaa gct atg taagggtatagc aggggaacagc actctagaag ctatgactca				960
Glu Lys Ala Met				
200				
attgagacta caagtaccac ggtgctactt gcacagaccc ctttggttaa atgtaaattc				1020
ttgtacaatt gaaggatacg cagaaggaca tctttctagt ctaacagtca ggagctgctc				1080
tggtcattcc cttgtatgaa ctggtctaaa gactgttagt ggggtgttag ttgatttttc				1140
ctggtatact gtttcttggc tgacactact ggtcaagtaa gaaatttgta aataaatttc				1200
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<212> DNA

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<220>

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<222> 101..355

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 seq LFLCYLLLFTCSG/VE

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 Met Arg Gln Lys Ala  
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 gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163  
 Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val  
 -15 -10 -5 1  
 gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211  
 Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly  
 5 10 15  
 ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259  
 Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Leu Ala Val  
 20 25 30  
 gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307  
 Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn  
 35 40 45  
 tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355  
 Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly  
 50 55 60 65  
 tagtggccac gctgcagagc ctcgggggctg gtggcagcag cgtcgtcata ggtaatatg 415  
 gtgccctgat gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475  
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 cctcaagtga tctcctgtgc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715  
 cccaraatcc araactttgt ctatcactct cccaacaac ctagatgtga aaacagaata 775  
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 ctgcagtggg aggagccctg gcagtggggg ctgtgccgtg gtgctcagtg cc atg ggc 178  
 Met Gly

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ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg      226
Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
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Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
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gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc      322
Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
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aac atc ctc ctg gcc tct gtt ggg tca gtg ttg ggg gcc tgc ttg ggg      370
Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
10 15 20
aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat      418
Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
25 30 35
gag gca aga gaa aat gta ccc caa ggt gaa cct cca aaa ccc cca ctc      466
Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
40 45 50 55
aag tca gag aaa cat gag gaa taaaggtcac atgcagatgc aaaaaaaaaa      517
Lys Ser Glu Lys His Glu Glu
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<210> 68
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<212> DNA
<213> Homo sapiens

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gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg      180
ttcatggttg gggatatttt ctcgactgc atg gaa tca gaa aga agc aaa agg      233
Met Glu Ser Glu Arg Ser Lys Arg
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atg gga aat gcc tgc att ccc ctg aaa aga att gct tat ttc cta tgt      281
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
-25 -20 -15
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Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
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Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
10 15 20
aat gcc aga tcc att cca cgc acc gtt cct cct gat gtt atc tca tta      425
Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu
25 30 35

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Phe Thr Pro Ser Leu Gln Leu Leu Phe Thr Ser Asn Ser Phe Asp	
55 60 65 70	
gtg atc agt gat gat gct ttt att ggt ctt cca cat cta gag tat tta	569
Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu	
75 80 85	
ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg	617
Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg	
90 95 100	
gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag	665
Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln	
105 110 115	
aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg	713
Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val	
120 125 130	
gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta	761
Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu	
135 140 145 150	
gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc	809
Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys	
155 160 165	
gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tcg	857
Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser	
170 175 180	
aag gat ttc gat tgc atc att aca gaa ttt gca aag tct caa gac ctg	905
Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu	
185 190 195	
cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag	953
Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu	
200 205 210	
tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa	1001
Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu	
215 220 225 230	
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Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val	
235 240 245	
tta agg gaa ata cac aga ttt aca aac atg tca tagttgactt aagcgcgcatga	1102
Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser	
250 255	
gacaccaaatt tctgtggctg ccatcagaaa ttttctacag tacatgaccc ggatgaactc	1162
aatgcatgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg	1222
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taagcgttta atgggtatctg ttactccaaa aagaaatatt aatatgtact tttccattta	1402
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aaaaaaaaa	1472

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 172..1449

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 <222> 172..255  
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 score 5.94825670923113  
 seq XVLLEPFVHQVGG/HS

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 gccgctggac tccgctgcct ccccatctc cccgccatct gcgcccggag g atg agc 177  
 Met Ser  
 cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 225  
 Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu  
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 ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 273  
 Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg  
 -10 -5 1 5  
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 Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln  
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 ttc tac gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac 369  
 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr  
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 aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg 417  
 Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu  
 40 45 50  
 tgt cta ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att 465  
 Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile  
 55 60 65 70  
 gta gat aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca 513  
 Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr  
 75 80 85  
 aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac 561  
 Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp  
 90 95 100  
 tgg gtg cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta 609  
 Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu  
 105 110 115  
 gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act 657  
 Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr  
 120 125 130  
 gta gag aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct 705  
 Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro  
 135 140 145 150  
 tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat 753  
 Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn  
 155 160 165  
 gca aag cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act 801  
 Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr  
 170 175 180  
 tcc cgc tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga 849  
 Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg  
 185 190 195  
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 Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln Ile Arg  
 200 205 210

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Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val Cys Gly
215      220      230
atg cag gtg tac caa gca ggc agt ggg cag ctc atg ttc atg aac aag      993
Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met Asn Lys
      235      240      245
tac cat gga cgg aag cta tct atg cag ggc ttc aag gag gca ctt ttc      1041
Tyr His Gly Arg Lys Leu Ser Met Gln Gly Phe Lys Glu Ala Leu Phe
      250      255      260
cag ttc ttc cac aat ggg cgg tac ctg cgc cgt gaa ctc ctg ggc cct      1089
Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu Gly Pro
      265      270      275
gtg ctc aag aag ctg act gag ctc aag gca gtg ttg gag cga cag gag      1137
Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg Gln Glu
      280      285      290
tcc tac cgc ttc tac tca agc tcc ctg ctg gtc att tat gat ggc aag      1185
Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp Gly Lys
      295      300      305      310
gag cgg ccc gaa gtg gtc ctg gac tca gat gct gag gat ttg gag gac      1233
Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu Glu Asp
      315      320      325
ctg tca gag gaa tca gct gat gag tct gct ggt gcc tat gcc tac aaa      1281
Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala Tyr Lys
      330      335      340
ccc atc ggc gcc agc tct gta gat gtg cgc atg atc gac ttt gca cac      1329
Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe Ala His
      345      350      355
acc acc tgc agg ctg tat ggc gag gac acc gtg gtg cat gag ggc cag      1377
Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu Gly Gln
      360      365      370
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Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile Val Thr
      375      380      385      390
gag ata agt gag gag agt ggg gag tgagcttgct agctgctcca gtacttgaga      1479
Glu Ile Ser Glu Glu Ser Gly Glu
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ggtggctcct gcagcctgga gctgatgtgc agtggcctct gtgagcccca gcctgagcca      1599
gtcccagctg tgcttgaggt ctttatttat tttaactatt tcttcaacat tccacatttg      1659
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<210> 70

<211> 1637

<212> DNA

<213> Homo sapiens

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<222> 30..1427

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<221> sig\_peptide

<222> 30..77

<223> Von Heijne matrix

score 3.71064775937629

seq YAAAAGVLAGVES/RQ

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Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val		
	10 15 20	
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Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser		
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gcc ggc ctc ctc cgt gcg gag aag aag ctg cgg ccg cac ctg gcc aag	245	
Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys		
	45 50 55	
gtg cta gtg tat gag ttg ttg ttg gga aag ggc ttt cga ggg ggt ggg	293	
Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly		
	60 65 70	
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Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala		
	75 80 85	
gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac	389	
Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp		
	90 95 100	
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Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp		
	125 130 135	
tat ttc aag aga caa ggt ttc tcc tat cag ggt cgg gct tcc agc ctc	533	
Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu		
	140 145 150	
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Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu		
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Met Pro Glu Leu Leu Val Phe Pro Ala Gln Thr Asp Leu His Glu His		
	170 175 180	
cca ctg tac cgg gcc gga cac ctc att ctg cag gac agg gcc agc tgt	677	
Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys		
	185 190 195 200	
ctc cca gcc atg ctg ctg gac ccc ccg cca ggc tcc cat gtc atc gat	725	
Leu Pro Ala Met Leu Leu Asp Pro Pro Pro Gly Ser His Val Ile Asp		
	205 210 215	
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Ala Cys Ala Ala Pro Gly Asn Lys Thr Ser His Leu Ala Leu Leu		
	220 225 230	
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Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu		
	235 240 245	
gca tcc atg gcc acg ctg ctg gcc cgg gct ggc gtc tct tgc tgt gaa	869	
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Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr		
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His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly	
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Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro	
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Arg Gly Leu Ser Thr Phe Pro Gly Ala Glu His Cys Leu Arg Ala Ser	
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Pro Glu Thr Thr Leu Ser Ser Gly Phe Phe Val Ala Val Ile Glu Arg	
395 400 405	
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Val Glu Val Pro Ser Ser Ala Ser Gln Ala Lys Ala Ser Ala Pro Glu	
410 415 420	
cgc aca ccc agc cca gcc cca aag aga aag aag aga cag caa aga gcc	1397
Arg Thr Pro Ser Pro Ala Pro Lys Arg Lys Arg Gln Gln Arg Ala	
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gca gcc ggt gct tgc aca ccg cct tgc aca tagcagaggc tccgggctga	1447
Ala Ala Gly Ala Cys Thr Pro Pro Cys Thr	
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cgcaggaagc agtttgggtt ttgaaagggtt attgggtccc ttccttgggc tgtgttcttg	1567
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<210> 71

<211> 1636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..1175

<220>

<221> sig\_peptide

<222> 30..77

<223> Von Heijne matrix

score 3.71064775937629

seq YAAAAGVLAGVES/RQ

<400> 71

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-15

-10

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Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val	
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tgc gaa acg cag cgc tac tcc gcc gtg ctg gat gct gtg atc gcc agc	197
Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser	
25 30 35 40	
gcc gcc ctc ctc cgt gcg gag aag aag ctg cgg ccg cac ctg gcc aag	245
Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys	
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Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly	
60 65 70	
ggc cga tgg aag gct ctg ttg gcc cgg cac cag gcg agg ctc aag gct	341
Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala	
75 80 85	
gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac	389
Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp	
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Leu Leu Glu Val Gly Ser Arg Pro Gly Pro Ala Ser Gln Leu Pro Arg	
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Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp	
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Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu	
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Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu	
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atg ccg gag ctg ctg gtg ttt ccc gcc cag aca gat ctg cat gaa cac	629
Met Pro Glu Leu Leu Val Phe Pro Ala Gln Thr Asp Leu His Glu His	
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cca ctg tac cgg gcc gga cac ctc att ctg cag gac agg gcc agc tgt	677
Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys	
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Leu Pro Ala Met Leu Leu Asp Pro Pro Pro Gly Ser His Val Ile Asp	
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gcc tgt gcc gcc cca ggc aat aag acc agt cac ttg gct gct ctt ctg	773
Ala Cys Ala Ala Pro Gly Asn Lys Thr Ser His Leu Ala Ala Leu Leu	
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aag aac caa ggg aag atc ttt gcc ttt gac ctg gat gcc aag cgg ctg	821
Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu	
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gca tcc atg gcc acg ctg ctg gcc cgg gct ggc gtc tct tgc tgt gaa	869
Ala Ser Met Ala Thr Leu Leu Ala Arg Ala Gly Val Ser Cys Cys Glu	
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Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr	
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cat gag gtc cac tac atc ctg ctg gat cct tcc tgc agt ggc tcg ggt	965
His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly	
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Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro
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Ser Ala Arg Arg Arg Met Lys Thr Trp Cys Glu Met Arg Cys Ser Arg
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Thr Arg Ala Pro Ser Gly
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Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Arg Leu Asn Asp
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Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
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ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
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Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly			
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His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr			
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 Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu  
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Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu  
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Asn Ile Glu Arg Ile Cys Phe Leu Leu Arg Lys Leu Val Leu Pro Glu							
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 <211> 1757  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 191..1468

<220>  
 <221> sig\_peptide  
 <222> 191..274  
 <223> Von Heijne matrix  
 score 4.02941490119842  
 seq GXLLEPFVHQVGG/HS

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<400> 76
catttttggtg cgagagaaac aataggacgg aaacgccgag gaacccggct gaggcggcag      60
cagagcatcc tggccagaac aagccaagga gccaagacga gagggacaca ctgacaaaaca      120
acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgccatctg      180
cgccccggagg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc      229
          Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg
                    -25                    -20

gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac      277
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His
-15                    -10                    -5                    1

tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc      325
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val
                    5                    10                    15

cca agg gaa cat cag ttc tac gag acc ctc cct tct gag atg cgc aaa      373
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys
                    20                    25                    30

ttc act ccc cag tac aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat      421
Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp
                    35                    40                    45

gaa gac agg aac ttg tgt cta ata gca tat cca ttg aaa ggg gac cat      469
Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His
50                    55                    60                    65

gga att gtg gac att gta gat aat tca gac tgt gaa cca aaa agt aag      517
Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys
                    70                    75                    80

ctc cta agg tgg aca aca aac aaa aaa cat cat gtc tta gaa aca gaa      565
Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu
                    85                    90                    95

aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg      613
Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met
100                    105                    110

aag agc cat aag tta gaa gaa gaa ttt gag tgg cta aag aaa tct gaa      661
Lys Ser His Lys Leu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu
115                    120                    125

gtc ttg tac tac act gta gag aag aag ggg aat ata agt tcc cag ctt      709
Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu
130                    135                    140                    145

aaa cac tat aac cct tgg agc atg aaa tgt cac cag caa cag tta cag      757
Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln
150                    155                    160

aga atg aag gag aat gca aag cat cgg aac cag tac aaa ttt atc tta      805
Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu
165                    170                    175

ctg gaa aac ctg act tcc cgc tat gag gtg cct tgt gtc ctt gac ctc      853
Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu
180                    185                    190

aag atg ggc aca cga caa cat ggt gat gat gct tca gag gag aag gca      901
Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala
195                    200                    205

gcc aac cag atc cga aaa tgt cag cag agc aca tct gca gtc att ggt      949
Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly

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210		215		220		225	
gtg cgt gtg tgt ggc atg cag gtg tac caa gca ggc agt ggg cag ctc							997
Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu							
	230		235		240		
atg ttc atg aac aag tac cat gga cgg aag cta tcg gtg cag ggc ttc							1045
Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe							
	245		250		255		
aag gag gca ctt ttc cag ttc ttc cac aat ggg cgg tac ctg cgc cgt							1093
Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg							
	260		265		270		
gaa ctc ctg ggc cct gtg ctc aag aag ctg act gag ctc aag gca gtg							1141
Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val							
	275		280		285		
ttg gag cga cag gag tcc tac cgc ttc tac tca agc tcc ctg ctg gtc							1189
Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val							
	290		295		300		305
att tat gat ggc aag gag cgg ccc gaa gtg gtc ctg gac tca gat gct							1237
Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala							
	310		315		320		
gag gat ttg gag gac ctg tca gag gaa tca gct gat gag tct gct ggt							1285
Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly							
	325		330		335		
gcc tat gcc tac aaa ccc atc ggc gcc agc tct gta gat gtg cgc atg							1333
Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met							
	340		345		350		
atc gac ttt gca cac acc acc tgc agg ctg tat ggc gag gac acc gtg							1381
Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val							
	355		360		365		
gtg cat gag ggc cag gat gct ggc tat atc ttc ggg ctc cag agc ctg							1429
Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu							
	370		375		380		385
ata gac att gtc aca gag ata agt gag gag agt ggg gag tgagcttgct							1478
Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly Glu							
	390		395				
agctgctcca gtacttgaga gcgactctgt gtcccaggca cagctgtgct gcgtcagggga							1538
ggaagccagt atggccagggt ggtggctcct gcagcctgga gctgatgtgc agtggcctct							1598
gtgagcccca gcctgagcca gtcccagctg tgcttgaggat ctttatattat tttaactatt							1658
tcttcaacat tccacatttg atgatgatac ctctttcttc cctgagtgtg tatgtttctaa							1718
tacaaatctt tttgtttatt gtaaaaaaaaa aaaaaaaaaa							1757

<210> 77  
 <211> 2027  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 48..950

<220>  
 <221> sig\_peptide  
 <222> 48..107  
 <223> Von Heijne matrix  
 score 6.64507667657896  
 seq LLPLLSLLVGAWL/KL

<400> 77  
 atgcgcagcg gggccgtggg tgtacgcggc gcagcgcggc agtcctg atg gcc cgg 56



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      275      280
aggagaaaaag ccttctaggg tcaactgtcat tccctggcca tgttgcaaac agcgcaattc 1030
caagctcgag agcttcagcc tcaggaaaga acttcccctt ccctgtctcc catcccctcg 1090
tggcaggcgc ctctcaccag ggcaggagag gactcagcct cctgtgtttt ggagaagggg 1150
cccaatgtgt gttgacgatg gctggggggcc aggtgtttct gttagaggcc aagtattatt 1210
gacacaggat tgcaaacaca caaacaattg gaacagagca ctctgaaagg ccatttttta 1270
agcattttta aatctattct ctcccccttt ctccctggat gattcaggaa gctgacattg 1330
tttcctcaag gcagaatttt cctgggttctg tttcttcagc cagttgctgt ggaaggagaa 1390
tgctttcttt gtggcctcat ctgtggtttc gtgtccctct gaaggaaact agtttcact 1450
gtgtaacagg cagacatgta actattttaa gcacagttca gtccataaag ggtctggggag 1510
aaccagatga tgtactaggt gaagcattgc attgtgggaa tcacaaagca aatagtactc 1570
cagaaagaca aatatcagaa gcttcctatt cttttttttt tttggagaca tttggagaca 1630
gggtctttct ctgttgccca ggctagagtg cactgggtgat cacggctcac tctagccttg 1690
aattcctggg cccaagcaat tctcccact cagcctcctg agtagctggg actacaagtg 1750
tgcaccacca tgccctggcta attttttgaa tttttgtagt gatgggatct cgctctgttg 1810
cccagggttg tctcgaactc ctggcctcaa gcgatcctcc cacctcgacc tcccaaagtg 1870
ctgggattac aggtgtgagc cacctcgctt gggccccctt ctccatatgc ctccaaaaac 1930
atgtccctgg agagtagcct gctcccacac tgtcactgga tgtcatgggg ccaataaaaat 1990
ctcctgcaat tgtgtatctc aaaaaaaaaa aaaaaaaa 2027

<210> 78
<211> 1880
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 156..512

<220>
<221> sig_peptide
<222> 156..206
<223> Von Heijne matrix
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      seq WLTAVASLLPSPG/NS

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atatacaggt ggcagctctc gtcccctgag agcggggcgaa ggccagggtc ccacactcgc 60
agcgtctgca cggcgctcgg gacctccctc gtccactgct tgagttccag aggtgggtgc 120
ttccctgtcc tgaacttcag agtgcgagat cataa atg ggt tcc ggc tgg ctt 173
                               Met Gly Ser Gly Trp Leu
                               -15

act gca gta gcc tcg ctc ctc ccc agc ccc ggt aac tcc gag cta ccc 221
Thr Ala Val Ala Ser Leu Leu Pro Ser Pro Gly Asn Ser Glu Leu Pro
-10 -5 1 5
gtc cag gcc ctc ggg cgt cgc ggg ggc agg gac tgg gcg cgg aac gag 269
Val Gln Ala Leu Gly Arg Arg Gly Gly Arg Asp Trp Ala Arg Asn Glu
10 15 20
gca ggg agg gac ctg gaa aaa cca ccc aga ttg cat tgc agt ggg cga 317
Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg Leu His Cys Ser Gly Arg
25 30 35
ggc cgc ctg gag gag ccg gtt ccc cct aac cac ctc ccc gtg ggg ctc 365
Gly Arg Leu Glu Glu Pro Val Pro Pro Asn His Leu Pro Val Gly Leu
40 45 50
tcg gtg cgc ggt tcc cag gtg ctc agc tct gct ggg ccc agg agg tgc 413
Ser Val Arg Gly Ser Gln Val Leu Ser Ser Ala Gly Pro Arg Arg Cys
55 60 65
cgc ctc aca ggg acg cgg aac ccc gtg cgt ggc ccc cgc cgg gtg gaa 461
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Arg Leu Thr Gly Thr Arg Asn Pro Val Arg Gly Pro Arg Arg Val Glu
70          75          80          85
cag ata gcg cgg ggc ggt ccg gag gct cgt cgc caa gca ggt gac tct      509
Gln Ile Ala Arg Gly Pro Glu Ala Arg Arg Gln Ala Gly Asp Ser
          90          95          100
tgc tgaaaaagtg gttggaacac ttaaggaaac ccggccccgc ctgtttctttc      562
Cys
taggtctttg gagtttggat taatcatttg tgtagcccg ttaggataaac cgaagacttt      622
attaaatcag cgcgtttaac aggaattccg cagtagtatac cacattagaa tcttgagtct      682
tggagttgaa catattcaca cagacttgcc ttcttcctgt ttagtttatg ccttggtgttc      742
cgttattgga acgctaagct tgtgggagtt gtttacatcc tactgctcaa ggtcatcgct      802
aaggtgtgat ttttcacaaa aagaatttgc aacctccggc atgaatgact taagggaagt      862
ctaatacccg tttctgattt tttttttttt ttaatttaaa agttaatctt tctgggocgg      922
gcgcggtggc tcacgcctgt aatcccagca ctttgggagg ccgaggcgga tcacgaggtc      982
aggagttcga gaccagcctg accaacaatgg tgaaaccccg tctctactaa aaacacaaaa      1042
attagccggg cggggtggcg cgcacctgta atcccagctg ctccgggaggc tgaggcagga      1102
gaatcgcttg aacctgggag gcgggggggt gcagtgagcc gagatctggc cattgcactc      1162
cagcgtgggc aacagagtga gactccatct caaaaaaaaaa ggttaatctt tccaactaga      1222
ttttcaagga tgaggatttt gttgttgttg ttgttgttgt tctcaaatgt attcccaggg      1282
cttggaaacag agcctgacat atactaggca ctcaacaaat atttgttgaa tgattgtaat      1342
gagtaacacc cattttttgca gatctttgtc ttctgagcct agggcatagg tcatcactgc      1402
aggggtgaga ttgtcaaaat gggagcttac aggtaattta agacttaaat gtttaaagag      1462
tatgtgctca ttcttcaaca aacttacttt tgtaaatta aaatggtaaa atgtggtgga      1522
ggggttgga tatatgtaat tcaagacagt tctgaatata aaaatgtttt actgtctatc      1582
accaccatct ataaatctaa ttcactaagg ataactctgt taaggtggct ggaaagaacc      1642
ttgaggagag aggcttattt aagtattggc tcaggaccac acctaaaatt ctcaaacagt      1702
tgagattctg ttgttttgtt ttttaagcgc agagacccaa gttgaggaa agcctataaa      1762
ataactggcc tgtactctta catacatgaa agccatcaaa gacaaaagact gaagaagaac      1822
ttttgcagat taaaggactt taagagacat gatcctgaac caaaaaaaaaa aaaaaaaaaa      1880

<210> 79
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..351

<220>
<221> sig_peptide
<222> 67..183
<223> Von Heijne matrix
      score 10.6473524146908
      seq FLCALCSFCPISA/AS

<400> 79
ctgattcttc gaaatgatat aagtcctgag ggcttcagtc ccattcgcg actcatactt      60
gcaatc atg gac tac agc cgt gtc ttt cag ggt gtg ttc ttc acc ttc      108
      Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe
          -35          -30
aag cat gct ttt gct gat ggt gct tgg gat ctt tca ttt ctc tgt gct      156
Lys His Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala
-25          -20          -15          -10
ctt tgc agt ttc tgc cca atc tca gct gcc tct ggc aga cct tac agg      204
Leu Cys Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg
          -5          1          5
tac ttg gaa ttc tgg aga tta tac ctg tct cct agt tcc atg gaa aat      252

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Tyr Leu Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn
      10      15      20
gga gtt caa aaa ttc cac gaa act ttt ttc att gtc ttt ttg ctt ttg      300
Gly Val Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu
      25      30      35
ttt gat atc gag agg aaa gga aaa agt tct gtt tgt cca ttt tgt tac      348
Phe Asp Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr
      40      45      50      55
aga taaggaaagt gggtttcacia aggttaagca acttggtcag tggtacccag      401
Arg
caaagagcag aatgattttc aacattcagt ttaaaagtcg gcgggggggca gtggctcaca      461
cctgtaatat cagcaacttg ggaggccaag gtggtacggt cgcttgaagc caaggagttc      521
aagaccagcc tgggtcaacat agcaaaacct tgtctttaca aaaagtaaaa aaaaaaaaaa      581
aaa      584

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<210> 80
<211> 1351
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 259..831

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<220>
<221> sig_peptide
<222> 259..375
<223> Von Heijne matrix
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      seq FCVCVIAIGVVQA/LI

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<400> 80
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gccagcagc tgcacagaag tgtacagagg cttctggcaa cacggattgc cgtctacctg      120
atgacctttc tcatcgtgac agtggcctgg gcagcacaca caaggttggt ccaagttggt      180
gggaaaacag acgacacact tgccctgctc aacctggccg catcatgggt gtgatgccct      240
ccctccctcc aggcctgc atg atg acc atc acc ttc ctg cct tac acg ttt      291
                Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe
                        -35                        -30
tcg tta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc ttg ttc      339
Ser Leu Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe
      -25      -20      -15
tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att gtg ggg      387
Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly
      -10      -5      1
tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag cgc tct      435
Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser
      5      10      15      20
gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc ctc caa      483
Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln
      25      30      35
ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc ttt gtc      531
Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val
      40      45      50
ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc tat gtc      579
Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val
      55      60      65
agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac agg gag      627

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Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu
 70          75          80
ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac gag cca      675
Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro
85          90          95          100
ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac gcc atc      723
Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile
          105          110          115
gtg gcc acg ctt ctc atc ctg gac atc tgc ccc tcc tgc tcc ctt tgg      771
Val Ala Thr Leu Leu Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp
          120          125          130
ctg gct gtt gct tcc ttc cag cgt ctg ctc ctc cgc ggc ctc atc tgc      819
Leu Ala Val Ala Ser Phe Gln Arg Leu Leu Arg Gly Leu Ile Cys
          135          140          145
ctc ttc gtc tgt tagagcgcgc gtctcgtctc agtcgtcacg tttttggttt      871
Leu Phe Val Cys
          150
ttgtgggggtt tttttttttt tttttttttg agacagtcct gctgtgtcgc ccaggctgga      931
gtatagtggc tcaagctcag ctcaactgcaa cctccgcctc ccaggttcaa gcaattctcc      991
tgctcagcc tccaagtag ttgggattac aagcaccac caccatgccc agctaacttt      1051
ttgcattttt aatagagatg aggtttcacc aagttggcca ggctgggtctt gaactcctga      1111
cctcaggtga tctgccacc tcggcctccc aaagtgtcgg gattacaggt gtaagccacc      1171
gtgcccggcc atcgtaatgt ttgaatttgc ttttttacat cttccatcct tttggagtgt      1231
cttgttccct cgtcatagtt cagcactgtg accaccttgg ggtagacac tatggtttta      1291
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<210> 81
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..377

<220>
<221> sig_peptide
<222> 111..233
<223> Von Heijne matrix
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      seq LWFLAQIPSRVAG/SL

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tgcggtctgag cgggcctccc atccctctta aaagagttag gcatttagcc atg cct      116
                                     Met Pro
                                     -40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc      164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
          -35          -30          -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag      212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
          -20          -15          -10
att ccc agt agg gtc gcc ggt agt ctt ctt tct gtc tgt gtg atg agc      260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser
          -5          1          5
aga gat ggt aac ata aag gac tct ggt gaa gac act cag tcg ggt acc      308
Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser Gly Thr

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10	15	20	25	
agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg	356			
Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg				
30 35 40				
cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag	407			
Leu Thr Phe Gln Arg Arg Phe				
45				
aggaacaagg ggctctggca gctcaaatca attaaccaag atccaattcc ctggagaatt	467			
tttaaccct cccactccac ccatcacttg cctggctaac atcagacact ggatcaaccc	527			
taaaaaggag tccatccaca gcatccaagg atccatagtg tcccctcaca ctgcagccac	587			
caatggaggc tactcccgaa agaaagatgg tggcttcttc tccacctagt gttgacagat	647			
ccctgaacta attatagtga aacatactgc ggcccacttc cattaatatag atttgtgcaa	707			
aaaaaaaaaaa aaa	720			

<210> 82  
 <211> 1029  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 223..432

<220>  
 <221> sig\_peptide  
 <222> 223..336  
 <223> Von Heijne matrix  
 score 4.17665217008018  
 seq LVNVLFFFFTPLMT/LV

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ccatatccac tcctaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt	180
cggcttgcac cacgtaccta tctcagctct ttttggaagc tt atg tcc tcc cca	234
Met Ser Ser Pro	
-35	
caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata	282
Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile	
-30 -25 -20	
tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg	330
Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu	
-15 -10 -5	
atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac	378
Met Thr Leu Val Thr Leu Ile Leu Val Trp Lys Val Thr Lys Asp	
1 5 10	
aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg	426
Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp	
15 20 25 30	
ctg cca taaagatctg gatctcttgg tggggactcc actgaggtga agacctgatt	482
Leu Pro	
gtacaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc	542
tgcttttagcc accctgttcc tccattgccat gatgtccccc caggcctcat ttccttcctc	602
tgccaccatc cctcttataa tgcactcctc ctgcggttct ttggtctgtc ccagcttctg	662
agtttgaatg tctttttttt tttttttttt tttttgkga tcttcaagac tgaaatagta	722
aatggctctt gatttctgca ctaacagagg aaagaaacaa gtacatggaa aagtaaaaat	782
tgattacaaa gcctaaattt tcctctataa attgggcatg tgctgactgt gggatattga	842
aattattggg agctcacagc atctcaagtt atataatgaa gctattcttg aagctcattt	902

ccagaagatc cttaaaatga aatggctcac tctctgctga attaatttgg agcaagttaa 962  
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aaaaaaaaa 1029

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tggtttccat ctcgttcact catgtagcct tcgctttgca aggtggag atg agg ggt 777  
Met Arg Gly  
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ccc act gct ggt cct tca gtt ctt tct gct gca cac ttg ctg gtc gta 825  
Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu Leu Val Val  
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ata ctg cct gca aac gcc gca ctc aag ctg ctg tct tgg gag aga ctg 873  
Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp Glu Arg Leu  
-5 1 5 10  
gcg gcc ccc gcc atc gag gtg gaa gta cct tcc aag gag gtg ctt gca 921  
Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu Val Leu Ala  
15 20 25  
gca ccc acc aag gcc aag cta ata ccc tct gag gat atg ttg gca gca 969  
Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met Leu Ala Ala  
30 35 40  
cct gcc atg gac ttg ctg gat tca ttt tct cct gga ttt ttg ata gct 1017  
Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe Leu Ile Ala  
45 50 55  
gct ccc gcc agc gct gtg atc act tgg cct ggg cct gca gat ttg gtt 1065  
Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala Asp Leu Val  
60 65 70  
gtt gct atg ctc ata gca cct gtt gca gga ctc att gct gcc cct gct 1113  
Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala  
75 80 85 90  
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Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
          110                      115                      120
gtg gat gga gaa gcc gca cta gcc gtt ccg tgg gag gca tgt tgg att      1257
Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
          125                      130                      135
ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggcttgt      1312
Pro Ser Pro Pro Ala
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agagcccagt ctcaactctga tcccccttctc tgtggagctc tgcagcctat accaagggga      1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctccctctctt      1432
atcctggagt taattcaagg gcttataatt agaagaacct gggtcgggtg tggaggctca      1492
cgctgtaat cccaacactt tgggaggcca aggagggcag atcgcttgag gccaggagtt      1552
caagaccagc cttgccaaca tagcaaaacc ccgactctac taaaaataca aaaaattagc      1612
tggacaggat ggcgcagccc tgtaatccca gctactcagt aggctgaggt aggagtatcg      1672
cttgaactcg gatggcggag gctgcagtga gccaaagactg cgccactcca ctgcactcca      1732
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                                Met Leu Pro Leu Leu Ile Ile Cys
                                -15                      -10
ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa      101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
          -5                      1                      5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca      149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
          10                      15                      20                      25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa      197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
          30                      35                      40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga      245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
          45                      50                      55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc      293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
          60                      65                      70
ttt act gag agg ctg aat aag ata tct gat ggg ctg aag gag aag gac      341
Phe Thr Glu Arg Leu Asn Lys Ile Ser Asp Gly Leu Lys Glu Lys Asp
          75                      80                      85

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ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac      389
Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
90                      95                      100                      105
ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg      437
Phe Leu Ser Cys Asn Asp Pro Thr Phe Cys Pro Ala Arg Asn Arg Arg
110                      115                      120
acc tcc ctg tgg gct gtg agt ctc agc agt gct cta ctc ctg gcc ata      485
Thr Ser Leu Trp Ala Val Ser Leu Ser Ser Ala Leu Leu Leu Ala Ile
125                      130                      135
gct gga gat gtt tct ttt act ggc aaa gga aga agg agg cag      527
Ala Gly Asp Val Ser Phe Thr Gly Lys Gly Arg Arg Arg Gln
140                      145                      150
taaagcagga acagggcagc cgcgatgtct tccagaagtg aacagaggcc gcagctacca      587
ccgtcacaaa gttcactcat ctctgggtcc cggtgacccc atccccccat accctccatc      647
ctgggtcctg gggcccaaaa gctctgaggc ctaggagact gcgctgtctc gtggtttgcc      707
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                        -15                      -10
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Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg Val Thr Lys Gly Ser Phe
                        -5                      1                      5
gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga      152
Glu Pro Gln Lys Cys Trp Lys Asn Asn Val Gly His Cys Arg Arg Arg
10                      15                      20
tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca      200
Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu Cys Arg Asn Lys Leu Ser
25                      30                      35
tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt      248
Cys Cys Ile Ser Ile Ile Ser His Glu Tyr Thr Arg Arg Pro Ala Phe
40                      45                      50                      55
cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac      296
Pro Val Ile His Leu Glu Asp Ile Thr Leu Asp Tyr Ser Asp Val Asp
60                      65                      70
tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt      344
Ser Phe Thr Gly Ser Pro Val Ser Met Leu Asn Asp Leu Ile Thr Phe
75                      80                      85
gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct      392
Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro

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90	95	100	
gag act act atg cca cca tcc gag gcc act act ccc gag act act atg			440
Glu Thr Thr Met Pro Pro Ser Glu Ala Thr Thr Pro Glu Thr Thr Met			
105	110	115	
cca cca tct gag act gct act tcc gag act atg cca cca cct tct cag			488
Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr Met Pro Pro Pro Ser Gln			
120	125	130	135
aca gct ctt act cat aat taattaacat ttacttctgg tatggaacaa			536
Thr Ala Leu Thr His Asn			
140			
ctagaaatac tgctggaaat aatatccaaa gagctgattc taccaatcca atttcaccag			596
gaaaattcca tcagggattg gatgaccatg gggatggaca taattgctac taccaacaca			656
acagccaaga gattgacctt acaattagaa atgtgtagac agaaatgtat agaagatata			716
aggattctct taattggact taaattcttt atctgtcttc ctccgatgta ctcaaatata			776
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atcttaatta ctctagcag ggataattag gtccctcttt ctcagattac aggc atg			117
			Met
gca aag atg ttt gat ctc agg acg aag atc atg atc ggc atc gaa agc			165
Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu Ser			
-30	-25	-20	
agc tta ctg gtt gcc gcg atg gtg ctc cta agt gtt gtg ttc tgt ctt			213
Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys Leu			
-15	-10	-5	1
tac ttc aaa gta gct aag gca cta aaa gct gca aag gac cct gat gct			261
Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp Ala			
5	10	15	
gtg gct gta aaa aat cac aac cca gac aag gtg tgt tgg gcc acg aac			309
Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr Asn			
20	25	30	
agc cag gcc aaa gcc acc acc atg gag tct tgt cca tct ctc cag tgc			357
Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln Cys			
35	40	45	
tgt gaa ggt tgt aga atg cat gcc agt tct gat tcc ctg cca cct tgc			405
Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro Cys			
50	55	60	65
tgt tgt gac ata aat gag gcc ctc tgacttggga aagctgggca caaaaatctt			459
Cys Cys Asp Ile Asn Glu Gly Leu			
70			
catgagcaat atttctttct taatagaatg ttttattatt caagtcaagt tctagagtgt			519

ttacatacta ttatataatg tacagtgtta ttttctgtac ttctgaataa atgtgcaata 579  
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 acttcaacct ccacctcccg agttctgcct cagcctccca agtagctggg attacaggtc 240  
 cagtcactcc acgcttcgag agtccaatta acaagagcaa gttctggtag aaagaagggtg 300  
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 Met Ser Asp Glu Asp Glu Ser  
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 Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Cys Leu Pro  
 -20 -15 -10 -5  
 cta gcc atc cca gcc gtg atc ttt tct tgc ctg aca aag aac tac aat 448  
 Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn  
 1 5 10  
 aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac 496  
 Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr  
 15 20 25  
 tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg 544  
 Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu  
 30 35 40  
 tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt 594  
 Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu  
 45 50  
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agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171  
Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly  
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agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219  
Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val  
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Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys  
5 10 15  
atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315  
Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln  
20 25 30  
gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363  
Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe  
35 40 45 50  
tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411  
Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val  
55 60 65  
gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467  
Gly Arg  
aggacagtga gtaatTTTTTg gataaggtat gctgaagaat ctcttcgaga agtctgatac 527  
atgatttttca tgTTaattgt aaatgttaat tccctcttgc aaggagagaca tatcctagat 587  
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aaacagcaca aaaaaatttc acttttgaaa tgaaattttt ataattgtat ggcaaaaggc 707  
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Met Ala  
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 aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229  
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile  
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 tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277  
 Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr  
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 Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly  
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 Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu  
 25 30 35 40  
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 Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln  
 45 50 55  
 aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469  
 Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu  
 60 65 70  
 gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517  
 Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala  
 75 80 85  
 acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565  
 Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His  
 90 95 100  
 cct tcc tct aag aaa att aag cac tgc aaa tta aag aag aag agt aaa 613  
 Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys  
 105 110 115 120  
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seq MLLGRLTSQLLRA/VP

<400> 93

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10 15 20
ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct      202
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser
25 30 35
ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg      250
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val Pro Arg
40 45 50
aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc tgc ttc      298
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe
55 60 65
ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa      346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln
70 75 80 85
tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg      394
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly
90 95 100
gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg      442
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu
105 110 115
aag atc cgc cgg cgg aag atg aac cac aag tac cgg aag ctg gtg      490
Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val
120 125 130
aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga      538
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg
135 140 145
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag      586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys
150 155 160 165
gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac      634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr
170 175 180
ctg cgg ggc aaa tgagtctggc gccgcccttc ccgccggttg ctgctgtgat      686
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<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..510

<220>

<221> sig\_peptide

<222> 247..318

<223> Von Heijne matrix  
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seq FCALEVVLPS CDC/RS

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gggaacattc tttaagcggg tcgtcttggc acgagacata aggcagttca acatcaagcc 120  
cttgccctga acagttccaa atgccaagaa ctggcgaatt actactttgg tttcaatggg 180  
tggtccaaaa ggatcatcaa gcttcaggag ctttctgacc ttgaagaaag ggaaaatgaa 240  
gatagc atg gtg cca ctt ccg aag caa agc ctg aag ttc ttc tgt gct 288  
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala  
-20 -15  
tta gaa gtg gtg ttg cca tcc tgt gat tgc agg agt cct ggc att ggc 336  
Leu Glu Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly  
-10 -5 1 5  
ttg gtg gag gag cct atg gat aag gtg gag gaa gga cca tta tca ttc 384  
Leu Val Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe  
10 15 20  
ctt atg aaa agg aag aca gcc cag aag ctt gct att cag aag gct ttg 432  
Leu Met Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu  
25 30 35  
tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc 480  
Ser Asp Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val  
40 45 50  
ttg atc atc ctt gaa gta ctt cag ttt cag taagcaaata aactcatttt 530  
Leu Ile Ile Leu Glu Val Leu Gln Phe Gln  
55 60  
gaaaagttaa ttgaataaaa atattgatat ctaaagcaaa aaaaaaaaaa aa 582

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<211> 1913  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 143..592

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<221> sig\_peptide  
<222> 143..277  
<223> Von Heijne matrix  
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seq VLVDLAILGQAYA/FA

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ggacatgagg ccagaccttg tgaccttggt ggcagtgggc agtggttga tgtgaggctc 120  
cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172  
Met Val Leu Met Trp Thr Ser Gly Asp Ala  
-45 -40  
ttc aag acg gcc tac ttc ctg ctg aag ggt gcc cct ctg cag ttc tcc 220  
Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser  
-35 -30 -25 -20  
gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag 268  
Val Cys Gly Leu Leu Gln Val Leu Val Asp Leu Ala Ile Leu Gly Gln  
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gcc tac gcc ttc gcc cca ccc cca gaa gcc ggc gcc cca cgc cgt gca 316



<400> 96  
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Met Ala Thr Ala Ser Pro Ser  
-15  
gtc ttt cta ctc atg gtc aac ggg cag gtg gag agc gcc cag ttt cca 101  
Val Phe Leu Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro  
-10 -5 1  
gag tat gat gac ttc tac tgc aag tac tgc ttt gtg tac ggc cag gac 149  
Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr Cys Phe Val Tyr Gly Gln Asp  
5 10 15 20  
tgg gcc ccc aca gcg ggt ctg gag gag ggg atc tca cag atc aca tcc 197  
Trp Ala Pro Thr Ala Gly Leu Glu Glu Gly Ile Ser Gln Ile Thr Ser  
25 30 35  
aag agc caa gat gtg cgg caa gca ctg gtg tgg aac ttc ccc att gat 245  
Lys Ser Gln Asp Val Arg Gln Ala Leu Val Trp Asn Phe Pro Ile Asp  
40 45 50  
gtc acc ttt aaa agc acc aac ccc tac ggc tgg cca cag atc gtg ctc 293  
Val Thr Phe Lys Ser Thr Asn Pro Tyr Gly Trp Pro Gln Ile Val Leu  
55 60 65  
agc gtg tat gga cca gat gtg ttc ggg aac gat gtg gtt cga ggc tat 341  
Ser Val Tyr Gly Pro Asp Val Phe Gly Asn Asp Val Val Arg Gly Tyr  
70 75 80  
ggg gcc gtg cac gtg ccc ttc tca cct ggc cgg cac aaa agg acc atc 389  
Gly Ala Val His Val Pro Phe Ser Pro Gly Arg His Lys Arg Thr Ile  
85 90 95 100  
ccc atg ttt gtc cca gaa tct acg tct aaa ctg cag aag ttt aca aga 437  
Pro Met Phe Val Pro Glu Ser Thr Ser Lys Leu Gln Lys Phe Thr Arg  
105 110 115  
tct gca agc tgc tcc acc cac tgaggacaaa tagaaacagg tcccctggga 488  
Ser Ala Ser Cys Ser Thr His  
120  
gtgctgagtc acgggggtcc cttcagccct gttccagcag cagaaggccg ggcgatttta 548  
ccctgtgccc tgtgaaaaat ctttgtgtct gagggggcag aggaaaaact cttgtcagat 608  
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aa 670

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<212> DNA  
<213> Homo sapiens

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<222> 1..336

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<222> 1..81  
<223> Von Heijne matrix  
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seq AHLCSDSLPEQQ/QD

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Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Ala Ala His  
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ctc tgc tcc gac agc ctc ccg gag tcc cag cag caa gac ggc aac cac 96

Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn His  
 -10 -5 1 5  
 gca ccc aac ttc tcc agc cac ggc tca tgc cgc cgt cgc cag cgg scc 144  
 Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg Xaa  
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 gac atg aca agg cgc tgc atg ccc gct agg cca ggt ttc ccc tca tcc 192  
 Asp Met Thr Arg Arg Cys Met Pro Ala Arg Pro Gly Phe Pro Ser Ser  
 25 30 35  
 cca gcc ccg ggg tgc tgc ccc ccg cgc tgc cat ctg aga ccc ggt agt 240  
 Pro Ala Pro Gly Ser Ser Pro Pro Arg Cys His Leu Arg Pro Gly Ser  
 40 45 50  
 acc gcc cat gct gca gcg gga aag aga aca gag agt cct ggg gac agg 288  
 Thr Ala His Ala Ala Ala Gly Lys Arg Thr Glu Ser Pro Gly Asp Arg  
 55 60 65  
 tac cgt gca gag ggc ttg aga agg ggc cgg gtc gcg ggg gca agg gta 336  
 Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val Ala Gly Ala Arg Val  
 70 75 80 85  
 tgaggggagg gctgcagacc gccgctcttc cagttcccg cctcctccgc gagctcaggc 396  
 gttggcattt cggggcctgg caaatccccg cccgcctcc gcgcaggggc tactgggagt 456  
 tggagtttgc ttctctgtag ttgggcagct gctcttggtc tagtgaccac cagcctggac 516  
 agctacggag aaccgcctt aggtagaaag aaagtgattt ttttcctttg caagagtttg 576  
 acccgggacc ctaactgctt aatgcatatt tagatcgttt tctgtacggt gtcagttcta 636  
 ctgatcctag tggtttagta atataaacct tttctatggt gtgggtgaaa ttatgtaacc 696  
 tgtgatgagg gaatcccttc cacgaattac tttgtagtcc agcgtgcacg ctagttcata 756  
 cttaaaagaa cttgcagatt tggaatgtga cgtgttttct ctttcagtaa cttcacgcct 816  
 ctccaagagg ctaatttttt tgtaaagatt ttgtgggagc tatgtaatga gatggggagt 876  
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 aaa 939  
  
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 <213> Homo sapiens  
  
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 <222> 174..443  
  
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 <222> 174..269  
 <223> Von Heijne matrix  
 score 4.13107367257584  
 seq SSLAFCQVGFLTA/QP  
  
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 ctagatgacc gactttaccc acttcaaagt ctaccttgac cctagcactc tctccaccct 120  
 gcatcctcac ctcagaccat cagttgggta ggccaacagc tcaccatcaa ttc atg 176  
 Met  
 ccc tgc cta gac caa cag ctc act gtt cat gcc cta ccc tgc cct gcc 224  
 Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro Ala  
 -30 -25 -20  
 cag ccc tcc tct ctg gcc ttc tgc caa gtg ggg ttc tta aca gca cag 272  
 Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala Gln  
 -15 -10 -5 1  
 cct tca cct ccg aga agg cgc aat ggg aaa gac aga tac acg ttg gtt 320  
 Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu Val

	5	10	15	
ctg caa cac cag gaa tgc cag gat gat tta gcc acc tcc tca ctt gtc				368
Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu Val				
	20	25	30	
tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt cga tgc aag cac caa				416
Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His Gln				
	35	40	45	
agc atc act gtt gct gac act aac aag tagtgccaag ggattgcctt				463
Ser Ile Thr Val Ala Asp Thr Asn Lys				
50	55			
taaggaagat caggagcgga acatctgggtg gcaaagaaaa tcttttctaag agccccattc				523
tagtgaccac cttcaacctc ctcatagcag gagagtttg gagtagggga cttaggatgt				583
tttgttcttt taatcaattc agaaaatatg tatgtttgaa ataaaaataa aaataacttga				643
gccaaaaaaa aaaaaaaa				661

<210> 99  
 <211> 647  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 282..521  
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 <221> sig\_peptide  
 <222> 282..386  
 <223> Von Heijne matrix  
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 seq LEPGLSSSAACNG/KE

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tgtgaaagaa tctcctgatg tcataatttc cgggtgtcac cggaacattt gatcatcatt	180
cctttggcaa ttccagcctt ctgtggaaag gccagtagaa agcattgatt tattcacctc	240
tacaggaatc agactcagcc tcttttgggt ttcagtgaag t atg cct ttt caa ttt	296
Met Pro Phe Gln Phe	
-35	
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att	344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile	
-30 -25 -20 -15	
gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag	392
Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu	
-10 -5 1	
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg	440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu	
5 10 15	
aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca	488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro	
20 25 30	
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg	541
Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys	
35 40 45	
tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct ggtaaacaaa	601
taaaagtggg ggcaccttta gatgatgaca aaaaaaaaaa aaaaaa	647

<210> 100

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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 251..643

<220>  
 <221> sig\_peptide  
 <222> 251..295  
 <223> Von Heijne matrix  
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 seq LLMFTQLLLCGFL/YV

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 ttcttgactt taattagtagt ctaggaaagt ctaaactttg gacctacctc tttttttgat 180  
 actcattttt gtacttttgc tctctgggat tggtttctta aagaatctgg atccttttta 240  
 atatgtcaaaa atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga 289  
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly  
 -15 -10 -5  
 ttt tta tat gtt cgg gtt gat gga tcg cgt ctt cgc cag gag gac ttt 337  
 Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe  
 1 5 10  
 ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc 385  
 Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly  
 15 20 25 30  
 gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc 433  
 Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr  
 35 40 45  
 att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat 481  
 Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp  
 50 55 60  
 ccc cgg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg 529  
 Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu  
 65 70 75  
 cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt 577  
 Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val  
 80 85 90  
 tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct 625  
 Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser  
 95 100 105 110  
 ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta 673  
 Leu Glu Val Ala Cys Lys  
 115  
 cttttattta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc 733  
 aatcaacaca ctgcataatt ttacttggtc ttcttcagag aagtctgggc aagatagtagt 793  
 caagccaggg tggtttagta agtttgttta tatgaaatca agatgaccaa tatgttatta 853  
 taagaaagca ggccggggcgc ggtggctcac gcctgtaatc ccagcacttt gggaggcgga 913  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 179..475

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 <221> sig\_peptide  
 <222> 179..295  
 <223> Von Heijne matrix  
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 seq PSLIAGLFGCLA/GY

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 gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca 178  
 atg gac ctg atc ggt ttt ggt tat gca gcc ctc gtg aca ttt gga agc 226  
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser  
 -35 -30 -25  
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 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly  
 -20 -15 -10  
 ctt ttt gtt gga tgt ttg gcc ggc tat gga gct tac cgt gtc tcc aat 322  
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn  
 -5 1 5  
 gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct 370  
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala  
 10 15 20 25  
 acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct 418  
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala  
 30 35 40  
 ggt ttg gtt gca ggt tta agc ctc atg atg atc ctg aga ctt gtc ttg 466  
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu  
 45 50 55  
 ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515  
 Leu Leu Leu  
 60  
 tgctgtaatg ggcagagcat attttttttg tattttaaag ataaacttca atatggaatg 575  
 ctagaaacac aaatagcact gtcacctcta atatgaacat tagtttgagg tagttttttt 635  
 ctaaagcaaa aatttttaact gtttttcta tgtcaagcac tatttttcatt aaaagtgtct 695  
 aatgaatcat gatatactct tccatttggt gtgtctatatt tttatatatt tggatatttt 755  
 tgaaaattcc aaatactcat gtctcaagta agcttaaact acaacttgtc acataaagga 815  
 agtcttaagt ggagttcaca gaatgataat gtatctatatt gtcatttggt ttatatttga 875  
 aattattaga aattatgctt tttccatttt aattgtattg ctgccagtgc tatttttttc 935  
 tttaaaaaat tttattctta gcacactggt atgtcctaac tgaatgtatt cagtattcaa 995  
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 aaaa 1059

<210> 102  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 34..327

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<221> sig\_peptide  
 <222> 34..162  
 <223> Von Heijne matrix  
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 seq LGDALLFLRPAGS/CA

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 Met Cys Glu Thr Leu Leu Thr  
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 agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt 102  
 Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly  
 -35 -30 -25  
 gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt 150  
 Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg  
 -20 -15 -10 -5  
 cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc 198  
 Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala  
 1 5 10  
 ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg 246  
 Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu  
 15 20 25  
 aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca 294  
 Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser  
 30 35 40  
 ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg 347  
 Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr  
 45 50 55  
 gcatcctgaa aacggccttc cttgtgtgta cattatttgc aacaagcaac aagtttataa 407  
 gcactttggg aaaattgcat gtgaggggta aaatattaaa gtcagtgcgt caacttgaaa 467  
 taaatgatga gttattgatt actgctaaag aaaaaaaaaa aaaaaaa 514

<210> 103  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 303..953

<220>  
 <221> sig\_peptide  
 <222> 303..359  
 <223> Von Heijne matrix  
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 seq LCCSGCVPSLCCS/SY

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 ttatctctaa cgttggaaaa cgatggagct aacacccatt atggagatta accacttttc 120  
 atcaggtttt taacttaagt cgtgaggaat acaacggtga acacaagatt cattttattt 180  
 tcatcaccat gggacgtatc ctgttgttga gttctctggg tcagacctct gaagacttct 240  
 cagatggatc ctagtctctg ggcttgccct gaaattactc gctgctcagg gagagagttg 300  
 aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tgc 347  
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser  
 -15 -10 -5  
 ctc tgt tgt tcc agc tat gtc ccc tct gtt gct cca act gca gct cat 395

Leu	Cys	Cys	Ser	Ser	Tyr	Val	Pro	Ser	Val	Ala	Pro	Thr	Ala	Ala	His	
				1				5					10			
tct	ggt	aga	ggt	cct	cat	tca	gct	ggt	cac	tgt	ggc	cag	agg	gtg	ttg	443
Ser	Val	Arg	Val	Pro	His	Ser	Ala	Gly	His	Cys	Gly	Gln	Arg	Val	Leu	
		15					20					25				
gcc	tgc	tcc	ctt	cct	caa	gta	ttc	tta	aag	cca	tgg	att	ttt	gtg	gag	491
Ala	Cys	Ser	Leu	Pro	Gln	Val	Phe	Leu	Lys	Pro	Trp	Ile	Phe	Val	Glu	
		30				35					40					
cat	ttt	tct	tcc	tgg	ctc	tcc	ctt	gag	tta	ttt	tcc	ttt	ctt	cgc	tat	539
His	Phe	Ser	Ser	Trp	Leu	Ser	Leu	Glu	Leu	Phe	Ser	Phe	Leu	Arg	Tyr	
				50						55					60	
ctt	ggg	act	ctt	ctt	tgt	gct	tgc	gga	cat	cgg	ttg	aga	gaa	gga	cga	587
Leu	Gly	Thr	Leu	Leu	Cys	Ala	Cys	Gly	His	Arg	Leu	Arg	Glu	Gly	Arg	
				65				70						75		
ctt	ctt	cct	tgt	ctc	ctt	ggt	ggt	ggc	tcg	tgg	ttg	ctc	ttc	aac	aac	635
Leu	Leu	Pro	Cys	Leu	Leu	Gly	Val	Gly	Ser	Trp	Leu	Leu	Phe	Asn	Asn	
		80						85					90			
tgg	act	gga	ggc	tct	tgg	ttt	tct	ctt	cat	ctt	caa	caa	gtc	agt	ctc	683
Trp	Thr	Gly	Gly	Ser	Trp	Phe	Ser	Leu	His	Leu	Gln	Gln	Val	Ser	Leu	
		95					100					105				
tct	caa	ggg	tct	cac	ggt	gca	gca	ttc	tta	cca	gag	gcc	att	ggg	cct	731
Ser	Gln	Gly	Ser	His	Val	Ala	Ala	Phe	Leu	Pro	Glu	Ala	Ile	Gly	Pro	
		110				115					120					
gga	ggt	cca	ggt	cca	gtg	tct	gga	gag	tcc	acc	tca	gct	cag	caa	tct	779
Gly	Val	Pro	Val	Pro	Val	Ser	Gly	Glu	Ser	Thr	Ser	Ala	Gln	Gln	Ser	
					130					135					140	
cat	gcc	ggt	tgg	caa	ttg	tca	gca	gaa	gcc	gat	gcc	tgc	cca	tca	ggt	827
His	Ala	Gly	Trp	Gln	Leu	Ser	Ala	Glu	Ala	Asp	Ala	Cys	Pro	Ser	Val	
				145					150						155	
ctt	tac	tct	gag	gtg	tta	gag	tgg	aat	aaa	aat	ata	aat	act	tat	act	875
Leu	Tyr	Ser	Glu	Val	Leu	Glu	Trp	Asn	Lys	Asn	Ile	Asn	Thr	Tyr	Thr	
				160				165						170		
agt	ttt	cat	gac	ttc	tgc	tta	ata	ttg	ggt	att	ttt	ktt	ggt	ttg	ttt	923
Ser	Phe	His	Asp	Phe	Cys	Leu	Ile	Leu	Gly	Ile	Phe	Xaa	Val	Leu	Phe	
		175					180					185				
tgt	ttt	ggc	ggt	gat	agg	ctt	acc	tta	cat	taaaccaggc	cttagccttt					973
Cys	Phe	Gly	Gly	Asp	Arg	Leu	Thr	Leu	His							
		190				195										
ctgtggccttt	ggtatggcaa	agcctcatat	tactctctag	tctgggttcag	caggacagtc											1033
aggccacac	ctggggctgt	ttgttttcta	cgtttacctc	aacataaggt	accttatcat											1093
tgtagcctt	catctcctga	tccaaaataa	aataaaatgc	cacaggtcaa	aaaaaaaaaa											1153
aaaaa																1158

<210> 104  
 <211> 1563  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 97..645

<220>  
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 <222> 97..156  
 <223> Von Heijne matrix  
 score 8.42885652997473  
 seq AVVGCLLVPPAEA/NK

<220>  
 <221> misc\_feature  
 <222> 972  
 <223> n=a, g, c or t

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 gtgtccggct ttgctggccc agcaagcctg ataagc atg aag ctc tta tct ttg 114  
 Met Lys Leu Leu Ser Leu  
 -20 -15  
 gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag 162  
 Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys  
 -10 -5 1  
 agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac 210  
 Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn  
 5 10 15  
 atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac 258  
 Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn  
 20 25 30  
 tgc ctg cac gtg gtg gag ccc atg cca gtg cct gcc cat gac gtg gag 306  
 Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu  
 35 40 45 50  
 gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc 354  
 Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr  
 55 60 65  
 acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg 402  
 Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu  
 70 75 80  
 ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag 450  
 Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys  
 85 90 95  
 ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat 498  
 Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp  
 100 105 110  
 gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca 546  
 Ala Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
 115 120 125 130  
 aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg 594  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu  
 135 140 145  
 cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc 642  
 Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu  
 150 155 160  
 agc tagatgggct ggtgtggttg ggtcaaggcc ccaacacccat ggctgccagc 695  
 Ser  
 ttccaggctg gacaaagcag ggggctactt ctcccttccc tcggttccag tcttcccttt 755  
 aaaagcctgt ggcatttttc ctcccttctcc ctaacttttag aaatgttgta cttggctatt 815  
 ttgattaggg aagaggggatg tgggtctctga tctctgttgt cttcttgggt ctttgggggt 875  
 gaagggaggg ggaaggcagg cccasaaggg aatggagaca ttcgaggcgg cctcaggagt 935  
 ggatgcgac ttgtctctcc tkggcctccc actcttngcc gccttccagc tctgagtctt 995  
 gggaatgttg ttacccttgg aagataaagy ctgggtcttc aggaactcag tgtctgggag 1055  
 gaaagcatgg cccagcattc agcatgtgtt cttttctgca gtgggttctta tcaccacctc 1115  
 cctcccagcc ccagcgctc agccccagcc ccagctccag ccctgaggac agctctgatg 1175  
 ggagagctgg gccccctgag cccactgggt cttcaggggt cactggaagc tgggtgttcgc 1235  
 tgtcccctgt gcacttctcg cactggggca tggagtgccc atgcatactc tgctgccggt 1295  
 cccctcacct gcacttgagg ggtctgggca gtcctcctc tcccagtggt ccacagtcac 1355  
 tgagccagac ggtcgggttg aacatgagac tcgaggctga gcgtggatct gaacaccaca 1415

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ccccctgtac ttgggttgcc tcttgtccct gaacttcggt gtaccagtgc atggagagaa 1475
aattttgtcc tcttgtctta gagttgtgtg taaatcaagg aagccatcat taaattgttt 1535
tatttctctc taaaaaaaaa aaaaaaaaaa 1563

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<210> 105
<211> 1621
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 80..820

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<220>
<221> sig_peptide
<222> 80..118
<223> Von Heijne matrix
      score 5.76690322882439
      seq MLVLRSA LTRALA/SR

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acctttccac tcgggaaacc ttcagaggag tctcagaaag gacacggctg gctgcttttc 60
tcagegcgca agccgcgcc atg ctc gtc ctc aga agc gcc ctg act cgg gcg 112
      Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
      -10 -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
      1 5 10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
      15 20 25 30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
      35 40 45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
      50 55 60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
      65 70 75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
      80 85 90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
      95 100 105 110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
      115 120 125
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
      130 135 140
ggg gga cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
      145 150 155
cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag 640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu
      160 165 170

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tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca      688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Trp Asn Glu Ser Ala
175                      180                      185                      190
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt      736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val
                      195                      200                      205
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat      784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn
                      210                      215                      220
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagttttcta      830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys
                      225                      230
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattgg tgcttaaatt      890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gttaatttgc tatgtttctt      950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctggtttac    1010
tttctgcatg gtatttcagt gtctgtcata cattaaaaat acttgctact gttttaagat    1070
cttgactctt catttgtttc agaatagctc ttctactgta ttctgacaac tctttgcttt    1130
atagcatttt gttgtattca aatgataatg gtagcatttc catgcttgtg acagcatttt    1190
taagttatta atatatttta tcaacctttc catcatgtct gttttcctgg ttttttttgg    1250
ttgttttttg accagtaaaa tttattttgt aataccaaat aggatttaag aaaattaacg    1310
tatttcttta ctatggaaaa ccacattgtc atttgtgaca tcatctatat taaatatggg    1370
tttcacatta gttatttgtc acttacttgg aaaatgatgc tgttaggtcc tggattataa    1430
aatctagaaa agacttggtg gtttatgtgc tgaaatgtct ttatttataa ttaattttta    1490
ctactattta ctttatttcg gatcctgttt aacaaagata cttgagacat ccatttggtt    1550
taatgaaatc tgtatggata tggaaatgct tgccctaata aaagcctaca tatacaaaaa    1610
aaaaaaaaaa a                                                              1621

<210> 106
<211> 557
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..388

<220>
<221> sig_peptide
<222> 77..217
<223> Von Heijne matrix
      score 4.57105404339594
      seq FLYLTLNQSCIFA/NY

<400> 106
aacaccctcc ctggaccctc tgccctggagg acggggaatc acagcagctg gtttggggtg      60
cctcccaaac caaaag atg ttc tct ccg cgc caa gct ttg acg ccc gac cc      112
                      Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro
                      -45                      -40
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt      160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe
-35                      -30                      -25                      -20
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt      208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys
                      -15                      -10                      -5
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag      256
Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu
                      1                      5                      10
ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg      304

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<210> 108  
 <211> 1129  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 81..986

<220>  
 <221> sig\_peptide  
 <222> 81..134  
 <223> Von Heijne matrix  
 score 5.03543461931947  
 seq ITLLGLAVNVVTT/LV

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<400> 108
acagcgcggc gggcgtctcg ctgctcgagc cgccgctgca gctctactgg acctggctgc      60
tccagtggat cccgctctgg atg gcc ccc aac tcc atc acc ctg ctg ggg ctc      113
                Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu
                -15                      -10

gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg      161
Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr
                -5                      1                      5

gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga      209
Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly
10                      15                      20                      25
ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga      257
Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg
                30                      35                      40

aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt      305
Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys
                45                      50                      55

gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct      353
Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala
                60                      65                      70

cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg      401
Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly
                75                      80                      85

atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg      449
Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met
90                      95                      100                      105
ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg      497
Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val
                110                      115                      120

att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat      545
Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr
                125                      130                      135

acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att      593
Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile
                140                      145                      150

ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa      641
Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu
                155                      160                      165

aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa      689
Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
170                      175                      180                      185

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gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat	737
Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr	
190 195 200	
ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag	785
Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln	
205 210 215	
tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg	833
Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met	
220 225 230	
gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg	881
Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu	
235 240 245	
caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat	929
Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His	
250 255 260 265	
caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat	977
Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn	
270 275 280	
aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct	1026
Asn Met Asp	
gtttcatgga aggagatatt aaacatttgt ttaattttta tttaagtgtt atacctattt	1086
cagcaaataa aatatttcat tgcttgaaaa aaaaaaaaaa aaa	1129

<210> 109  
 <211> 778  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 266..586

<220>  
 <221> sig\_peptide  
 <222> 266..307  
 <223> Von Heijne matrix  
 score 4.534746808071  
 seq ILVTVPGVCPAQC/CW

<400> 109	
tagatgtag aattggtatt tgttcttgct ttttggttgc gatggagtta tataactaagt	60
tacttatact aaggcattag tagtctcata tctgaggagc aattgtattt ttagttcagc	120
taaattaatg cctcttttta aatactaact tgtactactt ttgtggctgt gaatggtatc	180
ttttattgaa ctgaggcagc ttttaaaaga cttgcctgat catttagagc actcccattg	240
aggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg	292
Met Ile Leu Val Thr Val Pro Gly Val	
-10	
tgt cca gca caa tgt tgc tgg gca gag cag agg ggc aga ggc tca ggt	340
Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly	
-5 1 5 10	
atg tac ttc att gac aag tgg gca agg cca tcc tgg gta cca cat tgg	388
Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp	
15 20 25	
ctt aat gat ctc ttc att gtg aag tcc ggc tac ctc gtt tgc ata aga	436
Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg	
30 35 40	
act aca gta atc agg caa ggc att gtc aga att ggg agg aat aaa atc	484
Thr Thr Val Ile Arg Gln Gly Ile Val Arg Ile Gly Arg Asn Lys Ile	

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      45              50              55
agt gag tct gga agg agt gct ctg tat aca att gca aag aac aaa atg      532
Ser Glu Ser Gly Arg Ser Ala Leu Tyr Thr Ile Ala Lys Asn Lys Met
60              65              70              75
gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt      580
Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
      80              85              90
gga gtt tgaaaaggga ctattaatga aatctttctt ttccctcctt tctctttttc      636
Gly Val
ccttccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg      696
ctgcaatgat gttagctgtg gccactgtgg atttttcgca agaacattaa taaactaaaa      756
acttcaaaaa aaaaaaaaaa aa      778

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<210> 110
<211> 1301
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 59..745

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<220>
<221> sig_peptide
<222> 59..160
<223> Von Heijne matrix
      score 5.94384548075359
      seq LGAAALALLLANT/DV

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<400> 110
attcaaaacc aggctgaaga ttggaaggaa gttggccagc ctcggctgca ggacagaa      58
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30              -25              -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Leu Ala
      -15              -10              -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1              5              10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15              20              25              30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
      35              40              45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
      50              55              60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
      65              70              75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
      80              85              90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95              100              105              110

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agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
      115                      120                      125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
      130                      135                      140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
      145                      150                      155
ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac      682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
      160                      165                      170
cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag act ttg      730
Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
      175                      180                      185                      190
gcc tca gag aaa aaa tgattgtgtg aaactgccca gctcagggat aaccagggac      785
Ala Ser Glu Lys Lys
      195
attcacctgt gttcatggga tgtattgttt ccactcgtgt ccctaaggag tgagaaaccc      845
atttatactc tactctcagt atggattatt aatgtatttt aatattctgt ttagggccac      905
taaggcaaaa tagcccaaaa acaagactga caaaaatctg aaaaaactaat gaggattatt      965
aagctaaaaac ctgggaaata ggaggtttaa aattgactgc caggctgggt gcagtggctc     1025
acacctgtaa tcccagcact ttgggaggcc aaggtgagca agtcacttga ggtcggggagt     1085
tcgagaccag cctgagcaac atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc     1145
cgggtgtggt ggcaggcacc tgtagtccca gctaccggg aggctgaggc aggagaaatca     1205
cttgaacctg ggaggtggag gttgcggtga gctgagatca caccactgta ttccagcctg     1265
ggtgactgag actctaacta aaaaaaaaaa aaaaaa                                1301

<210> 111
<211> 1300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..676

<220>
<221> sig_peptide
<222> 59..160
<223> Von Heijne matrix
      score 5.94384548075359
      seq LGAAALALLLANT/DV

<400> 111
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atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30                      -25                      -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
      -15                      -10                      -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1                      5                      10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
      15                      20                      25                      30

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aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg	298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val	
35 40 45	
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc	346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser	
50 55 60	
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg	394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val	
65 70 75	
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc	442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe	
80 85 90	
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa	490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln	
95 100 105 110	
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac	538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr	
115 120 125	
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga	586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly	
130 135 140	
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg	634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg	
145 150 155	
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag	676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys	
160 165 170	
taaacctact ttctgttctg gaagctgcta agatgatcaa accacagact ttggcctcag	736
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tcattgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaacccat ttatactcta	856
ctctcagtat ggattattaa tgtatttttaa tattctgttt aggccacta aggcataata	916
gccccaaaac aagactgaca aaaatctgaa aaactaatga ggattattaa gctaaaacct	976
gggaaatagg aggttttaaaa ttgactgccg ggctgggtgc agtggctcac acctgtaac	1036
ccagcacttt gggaggccaa ggtgagcaag tcacttgagg tcgggagttc gagaccagcc	1096
tgagcaacat ggcgaaaccc cgtctctact aaaaatacaa aaatcaccgc ggtgtggtgg	1156
caggcacctg tagtcccagc taccggggag gctgaggcag gagaatcact tgaacctggg	1216
aggtggaggt tgcggtgagc tgagatcaca ccactgtatt ccagcctggg tgactgagac	1276
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<210> 112

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..278

<220>

<221> sig\_peptide

<222> 15..146

<223> Von Heijne matrix

score 12.2610572403264

seq PLFLLLLLLGSVTA/DI

<400> 112

gagaggagag gaga atg gcg gcg gaa ggc tgg att tgg cgt tgg ggc tgg  
Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp

50



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acacagaaca agggagggaa gaaaagctca gccttaaaca tagcaagggtg aaacctttgt 120
cctggggaat agtctggccc gctccttgga accacactca gactca atg gac tct 175
                                     Met Asp Ser
                                     -30
gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc 223
Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Arg Pro
                                     -25 -20 -15
ttg ctt tca tcc tgt ggc ctc cca cca agc act gcc tca gct gtg cgc 271
Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
                                     -10 -5 1
agg cta tgc tcc agg gga gtg tta aaa gga tca aat gaa aga agg gat 319
Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
5 10 15
atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tcg gac cga tac 367
Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
20 25 30 35
ctg gag agc cgc gat gcc tct cga ctg agt ggc cgg gac ccc tcc tca 415
Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp Pro Ser Ser
40 45 50
tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag 463
Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
55 60 65
ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag 511
Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
70 75 80
gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg 559
Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
85 90 95
aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag 607
Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
100 105 110 115
cag ggc aag ttc tgaaccagga gaggcagcct agacaaccaa gtggcagcag 659
Gln Gly Lys Phe
gtgggggcat tcttctagga atgaggggca tcagcccacc ccaggcacct cagtgggggtt 719
ccggggccacc tcaggactcc aagaggctgt gtggagccac cactcctagc cacagctgcc 779
atgataagtc cttccatgaa ggactgagga gggagagtgg ggggccaggg ctggtgctgc 839
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cggaaggcca agaaggcgct aagggggatg ggagggcagg ttttccaggc tggagtgggt 1499
tccaccact cgctgtcca caggcttcct tgtaagcaag tcagcagcac agctactcac 1559
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aaaaaaaaa aaaaaa 1634

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<210> 114  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 223..417

<220>

<221> sig\_peptide

<222> 223..270

<223> Von Heijne matrix

score 4.19788230215007

seq LACVRESTSVAWA/CK

<400> 114

ttagggggcc	tgtaacccag	cacgtgcatc	gggggctgtc	ccgggggtca	ggggagggag	60
gccagcgggc	mgtgtcgggg	tccgccccga	ccccatccac	gaccccgact	cctatccgat	120
cctatccccg	gccccgctcg	ggcctttccc	cttgccgcct	ggctcggtcg	gctcgacgag	180
cagtaagttc	gtagccgccc	tccgaagccg	ggcgtgcatg	gg atg gca	gag ttg	234
				Met Ala Glu Leu		

-15

gcg tgc	gtg cgt	gag tcc	acc agt	gtg gca	tggt gca	tgt aag	gtg cgc	282
Ala Cys	Val Arg	Glu Ser	Thr Ser	Val Ala	Trp Ala	Cys Lys	Val Arg	

-10

-5

1

gga ggg	act gca	cct tct	cca tca	ggg gca	gaa ggc	cac gtc	atg ctg	330
Gly Gly	Thr Ala	Pro Ser	Pro Ser	Gly Ala	Glu Gly	His Val	Met Leu	

aac aag	agc cga	gaa gta	gaa tcg	cca gtg	tca agc	cgt cca	cgt tgt	378
Asn Lys	Ser Arg	Glu Val	Glu Ser	Pro Val	Ser Ser	Arg Pro	Arg Cys	

25

30

35

ggg atg	ccc act	ggt ccc	cca gga	tca ctc	aag acc	ctg tgact	ttgtgg	427
Gly Met	Pro Thr	Val Pro	Pro Gly	Ser Leu	Lys Thr	Leu		

40

45

tcactgatga	gtggaccaag	tgaagtccac	aagatggctg	ctgtggctcc	aggcatcacg	487
tccacatgca	aatccatcca	gaggcaggaa	ctgggaatag	gcttggaggt	ggccaggaca	547
gcaagtgggc	tgtctgtata	aacctcccct	ccacttggga	aggaaaatca	ccccccaagt	607
cgattttctg	tccatcttat	tgatcagaga	gcgttataaa	ttcacccatt	aaataatctg	667
gacaagggga	aaaaaaaaaa	aaaaaa				693

<210> 115

<211> 784

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 166..732

<220>

<221> sig\_peptide

<222> 166..237

<223> Von Heijne matrix

score 6.60662787180923

seq KMHLLVLSGAWG/MQ

<400> 115

attattgggt	gggggaaacc	cacgagggga	cgcggccgag	gagggtcgct	gtccaccgga	60
gggcgtggga	gtgaggtacc	agattcagcc	catttggccc	cgacgcctct	gttctcggaa	120
tccgggtgct	gcggattgag	gtcccgggtc	ctaacggact	gcaag atg	gag gaa ggc	177
				Met Glu Glu Gly		

ggg aac	cta gga	ggc ctg	att aag	atg gtc	cat cta	ctg gtc	ttg tca	225
Gly Asn	Leu Gly	Gly Leu	Ile Lys	Met Val	His Leu	Leu Val	Leu Ser	

-20

-15

-10

-5

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ggt gcc tgg ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg      273
Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu
      1      5      10
ctt ttc cga agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa      321
Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys
      15      20      25
ctc ttc ccc ttc tac ttc cac atc tcc atg ggc tgt gsc ttc atc aac      369
Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Xaa Phe Ile Asn
      30      35      40
ctc tgc atc ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg      417
Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp
      45      50      55      60
gag gcc agc cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act      465
Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr
      65      70      75
gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc      513
Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala
      80      85      90
ctg caa acc gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc      561
Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly
      95      100      105
agc cac cag ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc      609
Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro
      110      115      120
aag tac agt gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc      657
Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser
      125      130      135      140
tct ctt tgc aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct      705
Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
      145      150      155
ggc ctt gcc ctg gaa ata agg agc ctc tagcatgggc cctgcatgct      752
Gly Leu Ala Leu Glu Ile Arg Ser Leu
      160      165
aataaatgct tctccaaaaa aaaaaaaaaa aa      784

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<210> 116
<211> 804
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 75..623

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<220>
<221> sig_peptide
<222> 75..215
<223> Von Heijne matrix
      score 8.34104221735598
      seq RLLLPCLVRMALC/AP

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<400> 116
agtacggtgg ccgacgggag tcagacgctg gggatgaatg aaggtgctgg gtgcaggatc      60
aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct      110
      Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro
      -45      -40
ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct      158
Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser

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-35	-30	-25	-20	
tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg				206
Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met				
	-15	-10	-5	
gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag				254
Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys				
	1	5	10	
aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att				302
Lys Leu Ile Leu Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile				
	15	20	25	
gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc				350
Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser				
	30	35	40	45
aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag				398
Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu				
	50	55	60	
tgc ggt ggc gtg atc tcg gct cac tgc aac ctc cac ctc ctg ggt tca				446
Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser				
	65	70	75	
agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg				494
Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr				
	80	85	90	
cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca				542
Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser				
	95	100	105	
cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg				590
Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu				
	110	115	120	125
cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgcctggcct				643
Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala				
	130	135		
atgtggtgga gtatttatta tacgtaggat gtgaatccct gaaatacaca ggcaaactaa				703
atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat				763
ttcaataaaaa gataattttt atacaaaaaa aaaaaaaaaa a				804

<210> 117  
 <211> 484  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 30..335

<220>  
 <221> sig\_peptide  
 <222> 30..71  
 <223> Von Heijne matrix  
 score 4.49063834776683  
 seq FLTALLWRGRIPG/RQ

<400> 117				
gcagagtctt gagcagcgcg gcaggcacc atg ttc ctg act gcg ctc ctc tgg				53
	Met	Phe	Leu	Thr
				-10
cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg ccg				101
Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg Pro				
	-5	1	5	10

cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag 149  
 Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu  
 15 20 25  
 atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg 197  
 Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg  
 30 35 40  
 gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag 245  
 Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu  
 45 50 55  
 gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att 293  
 Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile  
 60 65 70  
 gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc 335  
 Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser  
 75 80 85  
 taatcctgag tcgtcaccct tggattttat ggatcacgga gctgaccatc tttacctggt 395  
 cctggaactg aaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa 455  
 acaaacaac acaaaaaaaaa aaaaaaaaaa 484

<210> 118  
 <211> 985  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 21..752

<220>  
 <221> sig\_peptide  
 <222> 21..107  
 <223> Von Heijne matrix  
 score 3.61056351168286  
 seq FPLYLLNFLGLWS/WI

<400> 118  
 gttttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc 53  
 Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala  
 -25 -20  
 att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg 101  
 Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu  
 -15 -10 -5  
 tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc 149  
 Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe  
 1 5 10  
 act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc 197  
 Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe  
 15 20 25 30  
 agt aac ctg cag gag ttt gcg ggc ccc tcc ggg aaa ctc tcc ctg ctg 245  
 Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu  
 35 40 45  
 gaa gtg ggc tgt ggc acg ggg gcc aac ttc aag ttc tac cca cct ggg 293  
 Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly  
 50 55 60  
 tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg 341  
 Cys Arg Val Thr Cys Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu  
 65 70 75  
 atc aag agc att gca gag aac cga cac ctg cag ttt gag cgc ttt gtg 389

Ile	Lys	Ser	Ile	Ala	Glu	Asn	Arg	His	Leu	Gln	Phe	Glu	Arg	Phe	Val		
80						85				90							
gta	gct	gcc	ggg	gag	aac	atg	cac	cag	gtg	gct	gat	ggc	tct	gtg	gat	437	
Val	Ala	Ala	Gly	Glu	Asn	Met	His	Gln	Val	Ala	Asp	Gly	Ser	Val	Asp		
95				100					105					110			
gtg	gtg	gtc	tgc	acc	ctg	gtg	ctg	tgc	tct	gtg	aag	aac	cag	gag	cgg	485	
Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	Lys	Asn	Gln	Glu	Arg		
			115					120					125				
att	ctc	cgc	gag	gtg	tgc	aga	gtg	ctg	aga	ccg	gga	ggg	gct	ttc	tat	533	
Ile	Leu	Arg	Glu	Val	Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr		
			130					135					140				
ttc	atg	gag	cat	gtg	gca	gct	gag	tgt	tcg	act	tgg	aat	tac	ttc	tgg	581	
Phe	Met	Glu	His	Val	Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp		
			145					150				155					
caa	caa	gtc	ctg	gat	cct	gcc	tgg	cac	ctt	ctg	ttt	gat	ggg	tgc	aac	629	
Gln	Gln	Val	Leu	Asp	Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn		
			160					165				170					
ctg	acc	aga	gag	agc	tgg	aag	gcc	ctg	gag	cgg	gcc	agc	ttc	tct	aag	677	
Leu	Thr	Arg	Glu	Ser	Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys		
					180					185				190			
ctg	aag	ctg	cag	cac	atc	cag	gcc	cca	ctg	tcc	tgg	gag	ttg	gtg	cgc	725	
Leu	Lys	Leu	Gln	His	Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg		
			195					200					205				
cct	cat	atc	tat	gga	tat	gct	gtg	aaa	tagtgtgagc	tggcagttaa						772	
Pro	His	Ile	Tyr	Gly	Tyr	Ala	Val	Lys									
			210					215									
gagctgaatg	gctcaaagaa	tttaaagctt	cagttttaca	tttaaaatgc	taggtgggtg											832	
cctgtaatcc	caggtacttg	gaaggctgag	gcaggagaat	ctcttgaacc	cagaaggcga											892	
aggttgcaat	gaaccgagat	catgccattg	tactctagcc	tgggtgacaa	gagcaagact											952	
ccgtctcaaa	aaaaaataaa	aaaaaaaaaa	aaa													985	

<210> 119  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 185..715

<220>  
 <221> sig\_peptide  
 <222> 185..253  
 <223> Von Heijne matrix  
 score 9.49395175807817  
 seq SLLFICFFGESFC/IC

<400> 119																	
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cagctcctgg	tattttctgc	ttcccttcgt	aggggaattta	gttattttat	tttattat											120	
agctaattta	gctattttta	aatagctaaa	ttttagctac	ttttttttca	attgacaaag											180	
aagg atg tct	aat caa aga	cta ccg ctg	att ttt tct	ctg ttg ttt	atc											229	
	Met Ser Asn	Gln Arg Leu	Pro Leu Ile	Phe Ser Leu	Leu Phe Ile												
	-20		-15		-10												
tgc ttc ttc	ggg gag agt	ttc tgc att	tgt gat gga	act gtc tgg	aca											277	
Cys Phe Phe	Gly Glu Ser	Phe Cys Ile	Cys Asp Gly	Thr Val Trp	Thr												
	-5		1		5												
aag gtt gga	tgg gag att	ctt cca gaa	gaa gta cat	tat tgg aaa	gtt											325	

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Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val
  10          15          20
aag ggt tct cca tct cac tgc ctg cct tat ctt ctg gat aaa cta tgc      373
Lys Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys
 25          30          35          40
tgc gac ttt gct aac atg gat ata ttt cag ggt tgt tta tat ctc att      421
Cys Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile
          45          50          55
tat aat tta tta caa gct gtc ttc ttc gtc tta ttt gtt ttg tct gtg      469
Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val
          60          65          70
cat tac ctg tgg aag aaa tgg aag aaa cac caa aaa aag ctg aaa aag      517
His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys
          75          80          85
caa gcc tcc tta gaa aaa cct ggt aat gat cta gaa agc cca ttg atc      565
Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile
          90          95          100
aac aac att gac caa aca ctc cac aga gtg gca acc aca gca tca gtg      613
Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val
          105          110          115          120
ata tac aag atc tgg gag cac agg tct cac cat cct tcc tct aag aaa      661
Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys
          125          130          135
att aag cac tgc aaa tta aag aag aag agt aaa gaa gaa gga gcc aga      709
Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg
          140          145          150
aga tac taaataaatg catatgcaaa tgtagcttac tcaattatag atatcacaaa      765
Arg Tyr
agaaatctat catctaagga ttaaaaattg ttctttggaa acctttataa aaaaaaaaga      825
aaaaaaaaaaaa aaaa      839

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<212> DNA
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<220>
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<222> 54..527

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<223> Von Heijne matrix
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      seq ALXSLNLPPTVA/AP

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aacgtcatct aggagcaccg agcagcttgg ctaaaagtaa ggggtgctgtg ctg atg      56
                                     Met
gcc ctg tgc gca ctg acc cgc gct ctg ccs tct ctg aac ctg gcg ccc      104
Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala Pro
-20          -15          -10          -5
ccg acc gtc gcc gcc cct gcc ccg agt ctg ttc ccc gcc gcc cag atg      152
Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met
          1          5          10
atg aac aat gcc ctc ctc caa cag ccc tct gcc ttg atg ttg ctc ccc      200
Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro

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	15	20	25	
tgc cgc cca gtt ctt act tct gtg gcc ctt aat gcc aac ttt gtg tcc				248
Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser				
30	35	40		
tgg aag agt cgt acc aag tac acc att aca cca gtg aag atg agg aag				296
Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys				
45	50	55	60	
tct ggg ggc cga gac cac aca ggt gct gga aac gtg cgt aga aca gta				344
Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr Val				
65	70	75		
ggc cga gta tcc aac gtt gat cat aac aaa cgg gtc att ggc aag gca				392
Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys Ala				
80	85	90		
ggg cgc aac cgc tgg ctg ggc aag agg cct aac agt ggg cgg tgg cac				440
Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp His				
95	100	105		
cgc aag ggg ggc tgg gct ggc cga aag att cgg cca cta ccc ccc atg				488
Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro Met				
110	115	120		
aag agt tac gtg aag ctg cct tct gct tct gcc caa agc tgatatccct				537
Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser				
125	130	135		
gtactctaataaaaatgccccccccccctcaaaaaaaaaaaaaaa				583
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score 6.45239823575329				
seq SVFLLMVNGQVES/AQ				
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gcaacgccgg cgtctcttag caaccgcgcg cggcctagggt ggggtcccccc ggcacccccca				120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac				170
Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn				
-15	-10			
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc				218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys				
-5	1	5	10	
aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg				266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu				
15	20	25		
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa				314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln				
30	35	40		
gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac				362
Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn				
45	50	55		

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ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg      410
Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
60          65          70          75
ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc      458
Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
80          85          90
tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct      506
Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
95          100          105
acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc      554
Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
110          115          120
gag tac aca gac ccc aag gtg gtg gct cag ggt gaa gcc cgg gaa gct      602
Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
125          130          135
atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca      650
Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
140          145          150          155
ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc      696
Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
160          165
ctgaagcctc tagcctgtgg tgtgcacgta caagcctcag gccccatttg tccagcctgt      756
cagcagctgg gaaatactaa gtcaccctct tctggttatg ttttaattttc caatttttct      816
caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca      876
taccaccac ctagatttta ccattaccaa tttcctgttc cgtacttgta tattcacata      936
tatccaacta ttcattccctg cttcaatcca tcctattttt attgcatttc aaaataaact      996
gtgaaatcag gaaaaaaaaa aaaaaaaaaa      1024

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<210> 122
<211> 760
<212> DNA
<213> Homo sapiens

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<220>
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      seq ALGLALCSTKALS/VG

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gcctctccag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc acactggagg cagctgggtgg cacg atg ggg gac aga      176
                               Met Gly Asp Arg
                               -45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc      224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
-40          -35          -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg      272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu
-25          -20          -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct      320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro

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-10	-5	1	5	
ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc	368			
Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala Leu Ala Ala				
10 15 20				
ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc	416			
Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr				
25 30 35				
agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg	464			
Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg				
40 45 50				
ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct	512			
Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro				
55 60 65				
gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg	560			
Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp				
70 75 80 85				
cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat	608			
Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His				
90 95 100				
ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc	664			
Leu Cys				
accaccatcc caccctgcc ctgcccact tcccagggt ctcccttctg actcagtaaa	724			
gatcaccgct gcctccctca aaaaaaaaaa aaaaaa	760			

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<220>  
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ggagaaggca ggtcctcttt atgttttcgc agctggttca aggggtttgg ggttttctat	120
ctaggttaaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac	180
acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt	230
Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu	
-45 -40 -35	
cta cac ctc cct cgc cct gac act tcc acc agg ttg ctc ctc acc tcc	278
Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser	
-30 -25 -20	
gtc tct gct ttt atc ctc tta ctg ctc ctt tca gga cca gca gaa atg	326
Val Ser Ala Phe Ile Leu Leu Leu Leu Leu Ser Gly Pro Ala Glu Met	
-15 -10 -5	
tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct	374
Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala	
1 5 10 15	
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct	422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser	

	20	25	30	
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta				470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val				
	35	40	45	
aac ctt tgaaggtatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct				526
Asn Leu				
	50			
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa				586
aaaaaaaa				594

<210> 124  
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<220>  
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 <222> 16..297

<220>  
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 <222> 16..93  
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Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln	
	-25 -20 -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt	99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe	
	-10 -5 1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg	147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu	
	5 10 15
ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg	195
Gly Gly Met Gly Pro Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp	
	20 25 30
ctc ttt gcc tgg ttg ttt oca aga tgt act gtg cct ctt act ttc ggt	243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly	
	35 40 45 50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc	291
Phe Glu Asn Met Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro	
	55 60 65
agc act tagggaggcc gaggcgggag gatggcttga ggtccgtagt tgagaccagc	347
Ser Thr	
ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaaat tagccgggtg	407
tgggtggctcg tgcctgttgt cccagctgct ccggtggctg aggcgggagg atctcttgag	467
cttaggcttt tgagctatca tggcgccagt gcaactccagc gtgggcaaca gagcgagacc	527
ctgtctctca aaaacaaaaa aaaaaaaaaa aa	559

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 <222> 216..635

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       seq ITLVSAAPGKVIC/EM

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 gctcgccctga ctcccggcct cttgcgctcc taggggcgga gaagggtgcg ggctcttcgc 120  
 cctttgtgtc ctccctcttt cactaacttc tggactttcc agctcttccg aagttcgttc 180  
 ttgcgcaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag 233  
   Met Thr Ser Met Thr Gln  
   -40  -35  
 tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag 281  
 Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu  
   -30  -25  -20  
 aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg 329  
 Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val  
   -15  -10  -5  
 att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act 377  
 Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr  
   1  5  10  
 ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg 425  
 Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met  
   15  20  25  30  
 gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg 473  
 Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met  
   35  40  45  
 aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att 521  
 Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile  
   50  55  60  
 aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg 569  
 Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val  
   65  70  75  
 gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac 617  
 Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His  
   80  85  90  
 aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac 665  
 Thr Lys His Leu Gly Asn  
   95  100  
 ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg aaataaacta 725  
 gcaaaaaaaaa aaaaaaaaaa 744

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 <212> DNA  
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<220>  
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<222> 164..268  
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 ccaggagacc tacacagtgg cccacgagga gaatgtccgc tttgtgtccg aaggtagcga 120  
 gcggggccag aggggtgcggc ataggctgct gggtcgcaaa acc atg gac ccg gga 175  
 Met Asp Pro Gly  
 -35  
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223  
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe  
 -30 -25 -20  
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271  
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp  
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 Ser Pro Gly  
 ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380  
 ggtggcccag ccggtgaggg cgggccaagg cctgtgcagt acgtggagag gacccccaat 440  
 ccccggctgc agaactttgt gccattttac ctagacgagt ggtgggcgca gcagttcctg 500  
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560  
 tgtcgccagg agagaagcat ggcgccctgc ccacccactg cgcctggctg ggtgccggcc 620  
 acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggctgtccc 680  
 aaccaagctg ccatggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc 740  
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 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127  
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 <212> DNA  
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<220>  
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<220>  
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 <222> 68..190  
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 seq AYLLYILLTGALQ/FG

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 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu  
 -40 -35 -30  
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157  
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr  
 -25 -20 -15  
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205  
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu  
 -10 -5 1 5  
 ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct 253  
 Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser

	10	15	20	
tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga				301
Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly				
	25	30	35	
taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac				361
tgctagctct gctttttatg caggagaaaa gccagagtt cactgtgtgt cagaacaact				421
ttctaacaaa catttattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc				481
caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa				526

<210> 128  
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<220>  
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 <222> 179..427

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 <222> 179..298  
 <223> Von Heijne matrix  
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 seq CLVVVTMATLSLA/RP

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aatctaccca ggaacaaaac accagtgact gcagcagcag cggcagcgcc tcggttcctg	120
agcccaccgc aggctgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag	178
atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt	226
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly	
-40 -35 -30 -25	
acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc	274
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val	
-20 -15 -10	
acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag	322
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu	
-5 1 5	
gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag	370
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu	
10 15 20	
gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac	418
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn	
25 30 35 40	
aag agt aag taactgcccg gctccgatgg tccccgagag aggagcatgg	467
Lys Ser Lys	
agggaaagttc tgcctgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccg	527
cggcccttgc ctttccccgc tgtgtctact ttctgtactt tcaaacctga gaataaacca	587
gtgttgctgc acataaaaaa aaaaaaaaaa a	618

<210> 129  
 <211> 776  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> 22..297

<220>  
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 <222> 22..66  
 <223> Von Heijne matrix  
 score 4.68058603039206  
 seq VLAGSLLGPTSRS/AA

<400> 129  
 actgcggggac ccactgcgga t atg gct gtc ttg gct gga tcc ctg ttg ggc 51  
 Met Ala Val Leu Ala Gly Ser Leu Leu Gly  
 -15 -10  
 ccc acg agt agg tcg gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc 99  
 Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro  
 -5 1 5 10  
 cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag 147  
 Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln  
 15 20 25  
 cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc 195  
 Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile  
 30 35 40  
 aaa cgc aag aac aag cac ggc tgg gtc cgg cgc ctg agc acg ccg gcc 243  
 Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala  
 45 50 55  
 ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tcg ctg 291  
 Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu  
 60 65 70 75  
 agc cat tgaggatcgc gacgcagtcg gcggggaccc tcatggaagc atcgccctcg 347  
 Ser His  
 cctcggacct tgccctggcgc tttttttgca gggagctggg gagcaggaac gcctcggacc 407  
 tgagtgtctt ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt 467  
 aggtttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtacaaaga 527  
 acatccgtgt acccagtacc ctgactaccg actacctaca acccgctccct gcccctcct 587  
 gagttctttt gaagctgata tcaggcatcg gattattttt tctgtaaata tttcagaatg 647  
 tatctctcca agatgagagc tcattaaaag ataattacaa agcttatcac atccaaaaga 707  
 attatcaata attttgaaat attattaaac gtgtataaaa tgttcaaagt tcaaaaaaaaa 767  
 aaaaaaaaa 776

<210> 130  
 <211> 998  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 9..845

<220>  
 <221> sig\_peptide  
 <222> 9..134  
 <223> Von Heijne matrix  
 score 6.13963522287438  
 seq RSLALAAAPSSNG/SP

<400> 130  
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 Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly  
 -40 -35 -30

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ggg tgg cgg cgg ttc gag agg ctc tgg gcc ggc agt cta agc tct cgc      98
Gly Trp Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg
-25 -20 -15
agc ctg gct ctt gca gcc gca ccc tca agc aac gga tcc cca tgg cgc      146
Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg
-10 -5 1
ttg ttg ggc gcg ttg tgc ctg cag cgg cca cct gta gtc tcc aag ccg      194
Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro
5 10 15 20
ttg acc cca ttg cag gaa gag atg gcg tct cta ctg cag cag att gag      242
Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu
25 30 35
ata gag aga agc ctg tat tca gac cac gag ctt cgt gct ctg gat gaa      290
Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu
40 45 50
aac cag cga ctg gca aag aag aaa gct gac ctt cat gat gaa gaa gat      338
Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp
55 60 65
gaa cag gat ata ttg ctg gcg caa gat ttg gaa gat atg tgg gag cag      386
Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln
70 75 80
aaa ttt cta cag ttc aaa ctt gga gct cgc ata aca gaa gct gat gaa      434
Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu
85 90 95 100
aag aat gac cga aca tcc ctg aac agg aac cta gac agg aac ctt gtc      482
Lys Asn Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val
105 110 115
ctg tta gtc aga gag aag ttt gga gac cag gat gtt tgg ata ctg ccc      530
Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro
120 125 130
cag gca gag tgg cag cct ggg gag acc ctt cga gga aca gct gaa cga      578
Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg
135 140 145
acc ctg gcc aca ctc tca gaa aac aac atg gaa gcc aag ttc cta gga      626
Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly
150 155 160
aat gca ccc tgt ggg cac tac aca ttc aag ttc ccc cag gca atg cgg      674
Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg
165 170 175 180
aca gag agt aac ctc gga gcc aag gtg ttc ttc ttc aaa gca ctg cta      722
Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu Leu
185 190 195
tta act gga gac ttt tcc cag gct ggg aat aag ggc cat cat gtg tgg      770
Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp
200 205 210
gtc att aag gat gag ctg ggt gac tat ttg aaa cca aaa tac ctg gcc      818
Val Ile Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala
215 220 225
caa gtt agg agg ttt gtt tca gac ctc tgatgggccc agctgcctgt      865
Gln Val Arg Arg Phe Val Ser Asp Leu
230 235
ggacgggtgct cagacaagtc tgggattaga gcctcaagga cattgtgtga ttgcctcaca      925
tttgcaggta atatcaagca gcaaactaaa ttctgagaaa taaacgagtc tattaccaaa      985
aaaaaaaaaaa aaa      998

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<210> 131  
<211> 779  
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..578

<220>

<221> sig\_peptide

<222> 27..119

<223> Von Heijne matrix

score 4.50637135496675

seq TALMVGAASILLEG/RP

<400> 131

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atctttctgg actggccctg cagagg atg gca tgc acc act act gcc ccc gcc      53
                               Met Ala Cys Thr Thr Thr Ala Pro Ala
                               -30                               -25
cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct      101
Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
      -20                               -15                               -10
gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga      149
Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
      -5                               1                               5                               10
gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt      197
Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
                               15                               20                               25
ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg      245
Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
                               30                               35                               40
tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca      293
Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
                               45                               50                               55
gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct      341
Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
      60                               65                               70
gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tcg      389
Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
      75                               80                               85                               90
tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt      437
Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
                               95                               100                               105
ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag      485
Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
                               110                               115                               120
cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct      533
Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
                               125                               130                               135
act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg      578
Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
      140                               145                               150
tgaacttctg tcttgtttga gccatggttt cattctcttt ttcagccatg tagcctgtgc      638
tgtaactcag taccacatta gcaactagtg aaagtcaatg tgggtaaatt tgtcattctt      698
caggttagaa catttcttcc ttttattctt gtgttttttg ctaaataaac tgggaaatta      758
tagtaaaaaa aaaaaaaaaa a
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<210> 132

<211> 1025

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 408..710

<220>

<221> sig\_peptide

<222> 408..533

<223> Von Heijne matrix

score 5.66440183652506

seq QLCFHLSWLYSWA/SQ

<400> 132

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cacatgatta atccagtctg ggcatgacc tttcttccat ccaaaacaag gtgatgggaa 120
gacaaaaaca atagctacta caaacaatag gagtttataa ttatgtgctg atgtattcga 180
agatgtgttg acagtcgtga gtgtgtatcc taggaaaggc gagctggact ctgtctccat 240
gggtggctctc accccagggg cctaggaaca gcctgtcacc acacaattac ttttataacc 300
ctggagatga aaatctcctt gtcctcaaaa tacttccaga agaacaacca gatgggaagg 360
accttggttg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac 416
                                     Met Ala His
                                     -40
gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga 464
Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
                                     -35 -30 -25
ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg 512
Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
                                     -20 -15 -10
agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt 560
Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
                                     -5 1 5
att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt 608
Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
10 15 20 25
ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg 656
Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
30 35 40
gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac 704
Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
45 50 55
aga gac tgagagttgg tgctgggtgt tgtgggtggca gatgatatta cctgaagaag 760
Arg Asp
ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt 820
ccctgggtgtc ttcatcttcc tccgtctccc tgctgtccct taccctctgc ccaatctcat 880
tactcctggt ctggggaggt gccttctgag gatactccac tgggggtacc tgagcctgga 940
ttagaggggca gggggaggat attgcctagc caaagtgggt gttcaataaa gaaccatttg 1000
gagatggcaa aaaaaaaaaa aaaaaa 1025
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<210> 133

<211> 607

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..501

<220>  
 <221> sig\_peptide  
 <222> 247..306  
 <223> Von Heijne matrix  
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 seq LLLVTLVASTVPG/NS

<400> 133  
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 ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt 120  
 gggcttctga tgggtccctag aggtatcagc tactcagtca gaaaacatac atggggaaga 180  
 aactgaagtt catgccacaa actgtagcag ctttgggaaca gaagggacca gacaacctca 240  
 aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288  
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val  
 -20 -15 -10  
 gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336  
 Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala  
 -5 1 5 10  
 cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384  
 His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val  
 15 20 25  
 ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432  
 Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn  
 30 35 40  
 gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480  
 Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn  
 45 50 55  
 tgt tct cac ggg cag gcc ttt tgaaccaccc tggtacagaa caccaaccct 531  
 Cys Ser His Gly Gln Ala Phe  
 60 65  
 ggtgcttttag gctgtctgtg ccatttctag gcaatgaacg agtagttact gtaccaaccc 591  
 aaaaaaaaaa aaaaaa 607

<210> 134  
 <211> 774  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 333..602

<220>  
 <221> sig\_peptide  
 <222> 333..416  
 <223> Von Heijne matrix  
 score 4.79986448293481  
 seq VPALPLLSSLICMA/MV

<400> 134  
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 ctctgctgta tcaggattcg attcttgggtg ttaaacaaga caacgctgaa ggctcgggtgc 120  
 agcagccctg caaaggtttt tccagcgcctc ttgggaggtg ggctgtgccc tgcctggccc 180  
 acctggccca cctggcccac cattacctga agggaagcat gaacagcctt tgacgtggga 240  
 gtggcgactg ctgagaggga actgtctgta cacaagcaat gtacgcttat gggacctgag 300  
 tggagcccca acccagcag ggcgtgktct tc atg gct ttt cct ggc caa tct 353  
 Met Ala Phe Pro Gly Gln Ser  
 -25

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gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctc ctg tca      401
Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser
-20 -15 -10
agt ctc tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa      449
Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu
-5 1 5 10
gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg      497
Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg
15 20 25
cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag      545
Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys
30 35 40
gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat      593
Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn
45 50 55
att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg      642
Ile Arg Gly
60
aatccagaat aactctgaag aagccgagta acaggcatga agtgaagaga aatcgctgta      702
acaggaagac agcaaagcag atgctaataa ccacactatt taacgaactg gaaccaacaa      762
aaaaaaaaaa aa      774

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<210> 135
<211> 611
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 110..376

<220>
<221> sig_peptide
<222> 110..208
<223> Von Heijne matrix
      score 3.64796206065748
      seq LVPHSPLPGALSS/AP

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<220>
<221> misc_feature
<222> 347
<223> n=a, g, c or t

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<400> 135
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gcctgcgcag agccagaggc ctcagaagcc acaggaacat ggcctaggc atg gct cag      118
                               Met Ala Gln

cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca      166
Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr
-30 -25 -20 -15
gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct      214
Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro
-10 -5 1
ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg      262
Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu
5 10 15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg      310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala Pro Ala Arg

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20	25	30	
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc			358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu			
35	40	45	50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctgggggactt			406
Ile Pro Gly Gln Cys Pro			
55			
ctcagcgcca gccattggc gcctgcgttg cccgcatcca ggccctgcgg caggccctgt			466
gctagcgtgt tcgcaccagg aacgcagggtg ctgggctgtc ggggaggcct caggccacct			526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa			586
atgaattact gttcaaaaaa aaaaa			611

<210> 136  
 <211> 925  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 22..417

<220>  
 <221> sig\_peptide  
 <222> 22..66  
 <223> Von Heijne matrix  
 score 5.47092708754574  
 seq RVLCPAAGAVRA/LR

<400> 136			
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Met Asn Arg Val Leu Cys Ala Pro Ala Ala			
-15	-10		
ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt	99		
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu			
-5	1	5	10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa	147		
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu			
15	20	25	
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac	195		
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn			
30	35	40	
cct cac cgc tgg tcg gtg ggc cat acc atg gga aag gga cat cag cgg	243		
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg			
45	50	55	
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc	291		
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile			
60	65	70	75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga	339		
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg			
80	85	90	
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct	387		
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro			
95	100	105	
gag act cca gct gcc tac aga gcg aga act tgacggggtg cccgctgggg	437		
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr			
110	115		
ctggcaggaa gggagccgac agccgccctt cggatttgat gtcacgtttg cccgtgactg	497		
tcctggctat gcgtgcgtcc tcagcactga aggacttggc tgggtggatgg ggcacttggc	557		



<220>  
 <221> CDS  
 <222> 107..1618

<220>  
 <221> sig\_peptide  
 <222> 107..178  
 <223> Von Heijne matrix  
 score 6.19650168602189  
 seq LGLYSLVLSGALA/YA

<400> 138  
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 cagtgtgccca gggtccttg cggcctcctc aagcctgtc caggct atg ggc atc 115  
 Met Gly Ile  
 aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg 163  
 Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu  
 -20 -15 -10  
 agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa 211  
 Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln  
 -5 1 5 10  
 gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg 259  
 Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp  
 15 20 25  
 gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg 307  
 Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met  
 30 35 40  
 tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat 355  
 Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His  
 45 50 55  
 gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc 403  
 Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser  
 60 65 70 75  
 tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc 451  
 Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly  
 80 85 90  
 cct tgg tac ctg ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg 499  
 Pro Trp Tyr Leu Leu Leu Leu Leu Gly His Cys Val Gly Leu Tyr Val  
 95 100 105  
 gcc tcg ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc 547  
 Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala  
 110 115 120  
 agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg 595  
 Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly  
 125 130 135  
 ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc 643  
 Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly  
 140 145 150 155  
 agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt 691  
 Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys  
 160 165 170  
 gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc 739  
 Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser  
 175 180 185  
 ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc 787  
 Phe Tyr Leu Pro Phe Phe Phe Phe Gly Pro Ile Met Thr Phe Asp Arg  
 190 195 200  
 ttc cat gct cag gtg agc cag gtg gag cca gtg aga cgc gag ggt gag 835

Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg	Glu	Gly	Glu		
205						210					215						
ctg	tgg	cac	atc	cga	gcc	cag	gca	ggc	cta	agc	gtg	gtg	gcc	atc	atg	883	
Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val	Ala	Ile	Met		
220					225					230					235		
gcc	gtc	gac	atc	ttc	ttt	cac	ttc	ttc	tac	atc	ctc	act	atc	ccc	agc	931	
Ala	Val	Asp	Ile	Phe	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr	Ile	Pro	Ser		
				240					245					250			
gac	ctc	aag	ttc	gcc	aac	cgc	ctc	cca	gac	att	gcc	ctc	gct	ggc	cta	979	
Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu	Ala	Gly	Leu		
			255					260					265				
gcc	tat	tca	aac	ctg	gtg	tat	gac	tgg	gtg	aag	gcg	gcc	gtc	ctc	ttt	1027	
Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala	Val	Leu	Phe		
			270				275						280				
ggt	ggt	gtc	aac	act	gtg	gca	tgc	ctc	gac	cac	ctg	gac	cca	ccc	cag	1075	
Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp	Pro	Pro	Gln		
			285			290					295						
cct	ccc	aag	tgc	atc	acc	gca	ctc	tac	gtc	ttt	gcg	gaa	acg	cac	ttt	1123	
Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu	Thr	His	Phe		
					305					310					315		
gac	cgt	ggc	atc	aac	gac	tgg	ctt	tgc	aaa	tat	gtg	tat	aac	cac	att	1171	
Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr	Asn	His	Ile		
				320					325					330			
ggt	ggg	gag	cat	tcc	gct	gtg	atc	cca	gag	ctg	gca	gcc	aca	gtg	gcc	1219	
Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala	Thr	Val	Ala		
				335				340					345				
aca	ttt	gcc	atc	acc	aca	ctg	tgg	ctt	ggg	cct	tgt	gac	att	gtc	tac	1267	
Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp	Ile	Val	Tyr		
			350				355					360					
ctg	tgg	tca	ttc	ctt	aac	tgc	ttt	ggc	ctc	aac	ttt	gag	ctc	tgg	atg	1315	
Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu	Leu	Trp	Met		
						370					375						
caa	aaa	ctg	gca	gag	tgg	ggg	ccc	cta	gca	cga	att	gag	gcc	tct	ctg	1363	
Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu	Ala	Ser	Leu		
						385				390					395		
tca	gtg	cag	atg	tcc	cgt	agg	gtc	cgg	gcc	ctg	ttt	gga	gcc	atg	aac	1411	
Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly	Ala	Met	Asn		
				400					405					410			
ttc	tgg	gcc	atc	atc	atg	tac	aac	ctt	gtg	agc	ctg	aac	agc	ctc	aaa	1459	
Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn	Ser	Leu	Lys		
				415				420					425				
ttc	aca	gag	ctg	gtt	gcc	cgg	cgc	ctg	cta	ctc	aca	ggg	ttc	ccc	cag	1507	
Phe	Thr	Glu	Leu	Val	Ala	Arg	Arg	Leu	Leu	Leu	Thr	Gly	Phe	Pro	Gln		
				430			435					440					
acc	acg	ctg	tcc	atc	ctg	ttt	gtc	acc	tac	tgt	ggc	gtc	cag	ctg	gta	1555	
Thr	Thr	Leu	Ser	Ile	Leu	Phe	Val	Thr	Tyr	Cys	Gly	Val	Gln	Leu	Val		
						450					455						
aag	gag	cgt	gag	cga	acc	ttg	gca	ctg	gag	gag	gag	cag	aag	cag	gac	1603	
Lys	Glu	Arg	Glu	Arg	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Lys	Gln	Asp		
					465				470					475			
aaa	gag	aag	ccg	gag	taggagggag	cgggtagagg	gatgggctct	gctcagctat								1658	
Lys	Glu	Lys	Pro	Glu													
				480													
tcttgggcca	gatggggcct	gaccgataga	ataaaaagact	tttctacaac	aaaaaaaaaa											1718	
aaaaaaaa																1725	

<210> 139

<211> 1474

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 16..471

<220>  
<221> sig\_peptide  
<222> 16..93  
<223> Von Heijne matrix  
score 5.809301698725  
seq FCVCVIAIGVVQA/LI

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<400> 139
tacacgtttt cgtta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc      51
              Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe
              -25              -20              -15
ttg ttc tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att      99
Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile
              -10              -5              1
gta ggg tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag      147
Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln
              5              10              15
cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc      195
Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val
              20              25              30
ctc caa ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc      243
Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ile Phe Ser Leu Phe
              35              40              45              50
ttt gtc ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc      291
Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro
              55              60              65
tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac      339
Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His
              70              75              80
agg gag ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac      387
Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His
              85              90              95
gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac      435
Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr
              100              105              110
gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tgaggacccc      481
Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp
              115              120              125
gcgtcacctg cccagctat caggtggcca atgtgtcttg agtccttggc gtctcatcct      541
ggaaacccca gaaaggcaca ggggtcttgg ctccaccctc ctctggatgc cttagatgtt      601
gtgtgagggtc agggcagccc ccacttcagg gaggacaacc ttcccgcgcg cccctccctt      661
cccagcggccc cctcccttcc cagaggctcc caccccaagc acagccgagg atggggtgcc      721
aggggtgaggt cagcaccagc agccaactgc tctcctcact cctctcagag gggctcagca      781
gccatgggta tccccctgcc ccaggcctca cccctgcccc aacaccagcc cctcctagtc      841
cctagtccct cccattccct ccggtccct cccagtgcc cccatcgctt cgcagcccct      901
tctgetccct ttggctggct gttgcttcc tccagcgtct gctcctccgc ggccctcatct      961
gcctcttcgt ctgtagagc gcgcgtctcg tctcagtcgt cacgtttttg gtttttgtgg      1021
ggtttttttt tttttttttt tttgagacag tctgtctgtg tcgcccaggc tggagtatag      1081
tggctcaagc tcagctcact gcaacctcg cctcccaggt tcaagcaatt ctctgcctc      1141
agcctcccaa gtagttggga ttacaagcac ccaccaccat gccagctaa ctttttgcac      1201
ttttaataga gatgagggtt caccaagttg gccaggctgg tcttgaactc ctgacctcag      1261

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gtgatctgcc cacctcggcc tcccaaagtg ctgggattac aggtgtaagc caccgtgccc 1321
ggccatcgta atgtttgaat ttgctttttt acatcttcca tccttttgga gtgtcttggt 1381
ccctcgcat agttcagcac tgtgaccacc ttggggtagt acactatggg tttatatcct 1441
gtacttgata ttctccaaaa aaaaaaaaaa aaa 1474

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<210> 140
<211> 653
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 222..374

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<220>
<221> sig_peptide
<222> 222..299
<223> Von Heijne matrix
      score 4.28353322771141
      seq ILFKFSLCPYAAA/LS

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<400> 140
taataatggtt gttaaattat tgccttctca tctgcgtgtc tcttatgttc tgcttaaaga 60
gattgtcagt ttgttcaagc tcttttttagt tggtgctcct ccagtgccta gctttgagct 120
ttgtacacgg tagttattga gttgagtaac atagtttggt ctgagtcatt tgtccacat 180
gcttgaagac ttggcttaac ctagtagata ataggaaaga a atg gaa atg ctc ttt 236
                                         Met Glu Met Leu Phe
                                         -25
gat gaa aga gcc cct ctc tta ttc atc ctt ttt aaa ttt tct ttg tgc 284
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe Lys Phe Ser Leu Cys
-20 -15 -10
cca tat gca gca gct ctc agc aaa cct ata ttt ggc agt gtg gcc tgt 332
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe Gly Ser Val Ala Cys
-5 1 5 10
atg act aaa gaa atc ctg gcc agg cac ggt ggc tca cgc ctg 374
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly Ser Arg Leu
15 20 25
taatcccagc actttgggag gccgaggcgg gtggattacg aggtcaggag attgagacca 434
tcctggctaa catggcgaaa ccccatctct acgaaaaata caaaaaaaaaa aattagccgg 494
gcatcatggc gggcgctgt agtcttagct actcaggagg ctgaggcagg agaatggcgt 554
gaacccggga ggcggagctt gcagtgagcc gagattgcgc cactgcactc cagcctgggg 614
caacagagca agactccgtc tcaaaaaaaaa aaaaaaaaaa 653

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<210> 141
<211> 1490
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 59..274

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<220>
<221> sig_peptide
<222> 59..127
<223> Von Heijne matrix
      score 7.37647149292058
      seq LGLCSLLVGAEAE/PS

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<400> 141
agacagaggc agggcttgcg acggaagtgg cctctctgct tctgcagggc tggggaag      58
atg ctg cgt cca gcg tta ccg tgg ctg tac ctt ggc ctc tgc agc ctc      106
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
-20 -15 -10
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg      154
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
-5 1 5
agc cgg ccg tac gcg gtg ctg cga ggg cag aac ctg gtg ttg atg gga      202
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
10 15 20 25
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt      250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
30 35 40
gtc tac aag ccc att ccg cgt ccg tgacagccag acaagttctt caatgagtat      304
Val Tyr Lys Pro Ile Arg Arg Arg
45
ttgggaatag gataagttgt gttgcacaca ggccagtggg gaagttggaa ccaaaacttt      364
cctactttga aatgaccttt ggtctggaca gttggtaaata gctaaatgaa ttagaagaaa      424
acatgtacta gacattattt tttcctaaca ctgtagcgca aataattggc ccctgagtc      484
gcttctcagt gtttctgact gtacttggtta aaagtaagac ctgaaagctc caaagggtcag      544
tgtaaagatg gagtggtcat gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa      604
ccacactgta aagaactcat cattaatgct tgaaaatggt attaagaagg agacttacca      664
tgcagacatt ccctatttaa gaaccatttg gttacagtgg gttaagaatc acagattttt      724
ttttttaatc tcacctgagt tagcctagaa tgcgctgggt gcaaagtggg gtcagctgtg      784
gggatcttgg gccctcggtc ctcacctgca tcctgccttg cactcaggtg ctccccctga      844
agtcagggtc acatcaggta gacctgttac tatatgcacc tttggcctgg aatgctctga      904
agttggactg gaaatggtac taggttggcc tgttacaaaa aggaccccat cctgcttaaa      964
cacattgata tcacctgccc tgcatttgag tctttctagc ccacgggtctg aaacttgagg      1024
cagctttcca gatttggaaat gtaaaaggct cagtgggcac tctgttcac cctgggtggg      1084
gagggccag ccaacagaag tgcattgtcca ctgtgcgggc cagtgtgtgt ttacacaaat      1144
ttcatctcag ctttgaaaat gctgctatta gtttccactg ttggtgaact ggattttttc      1204
ctcctattga aatgatactt tcatacttat aaagctgtcg tcaatattta tttcaagggtg      1264
ctagatttaa ttttggttatt aaattgaaat gcttatcttg tgttcaagca cagcactgat      1324
ttaacaacc tgcatttaat gtgaagtaac cgaagtagga tactgtaact gtgtaaggat      1384
tttgtttgta atcttgtaac attgaaccat tgaaatgttc agttctttgc ttttgagcaa      1444
aacgtcaatt aaaactaaag taaaatctta aaaaaaaaaa aaaaaa      1490

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<210> 142
<211> 661
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 158..442

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<220>
<221> sig_peptide
<222> 158..301
<223> Von Heijne matrix
score 7.53908709538105
seq FVILLLFIFTVVS/LV

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<400> 142
aaaaacagac gataccatcg cttcagcagc atcctctcag acaagagcca ctattttctga      60
ttcagatcac ctgtcatcga agtttaaaga aggggaaaca ggagacagaa atacactgaa      120

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ccaaaaagat tcaaaagagc aagtggaatc tctaaga atg gct tcc agc cac tgg      175
                                   Met Ala Ser Ser His Trp
                                   -45
aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa      223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln
-40 -35 -30
aaa att tac cct ttc cat gac aac tgg aac act gcc tgc ttt gtc atc      271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile
-25 -20 -15
ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc      319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe
-10 -5 1 5
ctt tat gaa gtg ctt gac tgc tgc tgc tgt gta aaa aac aaa acc gtg      367
Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val
10 15 20
aaa gac ttg aaa agt gaa ccc aac cct ctt aga agt atg atg gac aac      415
Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn
25 30 35
atc aga aaa cgt gaa act gaa gtg gtc taacactcta tagaagatga      462
Ile Arg Lys Arg Glu Thr Glu Val Val
40 45
acaaaatctc tgaagcagc tcaacctctt ctgagaaaaa aaatatattc tgaggccaac      522
tggttgetaca aaacaaattc tgactgaatg tttaaaacat ttctagtaga aggggaaaaa      582
aaagttaaac atgcactgtt tgtgtgtata gccatttcat taaatataca gtaaaacttc      642
ataaaaaaaaa aaaaaaaaaa      661

<210> 143
<211> 1789
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..454

<220>
<221> sig_peptide
<222> 5..64
<223> Von Heijne matrix
score 6.64507667657896
seq LLPLLSLLVGAWL/KL

<400> 143
cctg atg gcc cgg cat ggg tta ccg ctg ctg ccc ctg ctg tcg ctc ctg      49
Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu
-20 -15 -10
gtc ggc gcg tgg ctc aag cta gga aat gga cag gct act agc atg gtc      97
Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val
-5 1 5 10
caa ctg cag ggt ggg aga ttc ctg atg gga aca aat tct cca gac agc      145
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
15 20 25
aga gat ggt gaa ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc      193
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
30 35 40
atc gac ata ttt cct gtc acc aac aaa gat ttc agg gat ttt gtc agg      241
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
45 50 55

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gag aaa aag tat cgg aca gaa gct gag atg ttt gga tgg agc ttt gtc	289
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val	
60 65 70 75	
ttt gag gac ttt gtc tct gat gag ctg aga aac aaa gcc acc cag cca	337
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro	
80 85 90	
atg aag gtc aag ttt acc cat ggg gga act ggt tcc agc caa acc gca	385
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala	
95 100 105	
cca acc tgt ggc agg gaa agt tcc cca agg gag aca aag ctg agg atg	433
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met	
110 115 120	
gct tcc atg gag tct ccc cag tgaatgcttt ccccgcccag aacaactacg	484
Ala Ser Met Glu Ser Pro Gln	
125 130	
ggctctatga cctcctgggg aacgtgtggg agtggacagc atcacccgtac caggctgctg	544
agcaggacat gcgcgtcctc cgggggggcat cctggatcga cacagctgat ggctctgcca	604
atcacccgggc ccgggtcacc accaggatgg gcaacactcc agattcagcc tcagacaacc	664
tgggtttccg ctgtgctgca gacgcaggcc ggccgcccagg ggagctgtaa gcagccgggt	724
ggtgacaagg agaaaagcct tctagggtca ctgtcattcc ctggccatgt tgcaaacagc	784
gcaattccaa gctcgagagc ttcagcctca ggaaagaact tccccttccc tgtctcccat	844
ccctctgtgg caggcgctc tcaccagggc aggagaggac tcagcctcct gtgttttgga	904
gaaggggccc aatgtgtgtt gacgatggct gggggccagg tgtttctgtt agaggccaag	964
tattattgac acaggattgc aaacacacaa acaattggaa cagagcactc tgaaaggcca	1024
ttttttaagc attttaaaat ctattctctc cccctttctc cctggatgat tcaggaagct	1084
gacattgttt cctcaaggca gaattttcct ggttctgttt tctcagccag ttgctgtgga	1144
aggagaatgc tttctttgtg gcctcatctg tggtttcgtg tccctctgaa ggaaactagt	1204
ttccactgtg taacaggcag acatgtaact atttaaagca cagttcagtc ctaaaagggt	1264
ctgggagaac cagatgatgt actaggtgaa gcattgcatt gtgggaatca caaagcaaat	1324
agtactccag aaagacaaat atcagaagct tcctattctt tttttttttt tttttttttt	1384
ttgagacagg gtctttctct gttgcccagg ctagagtgca ctggtgatca cggctcactc	1444
tagccttgaa ttcttgggcc caagcaattc tcccacctca gcctcctgag tagctgggac	1504
tacaagtgtg caccaccatg cctggctaatt tttttgaatt tttgtagtga tgggatctcg	1564
ctctgttgcc cagggtgggc tccaactcct ggccctcaagc gatectccca cctcgacctc	1624
ccaaagtgtg gggattacag gtgtgagcca cctgcgctgg gcccccttct ccatatgcct	1684
ccaaaaacat gtccctggag agtagcctgc tcccacactg tcactggatg tcatggggcc	1744
aataaaatct cctgcaattg tgtatctcaa aaaaaaaaaa aaaaa	1789

<210> 144  
 <211> 2006  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 241..1302

<400> 144	
tagtgccgga gccccgccag agcccgactt cagccccagc cagatcccgc gtcaacggag	60
gcggaacggc ggaccccgta ccctggcagc atcggagcac cggcgggtga aggcaaggct	120
cctggactgg tcatatacct cttgtggccc tggcagaatc aagatgaggc cctgtcatgc	180
ctccccagtg aggcctacag tctgagcaga cagcatggcc tgccactggc agtgaacacc	240
atg tct gca gga ggt ggc cgg gcc ttt gct tgg caa gtg ttc ccc ccc	288
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro	
1 5 10 15	
atg ccc act tgc cgg gtc tat ggc aca gtg gca cac caa gat ggg cac	336
Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His	
20 25 30	

ctg ctg gtg ttg ggg ggt tgt ggc cgg gct gga ctg ccc ctg gac act	384
Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr	
35 40 45	
gct gag aca ctg gac atg gcc tcg cac aca tgg ctg gca ctg gca ccc	432
Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro	
50 55 60	
ctg ccc act gcc cgg gct ggt gca gct gcg gta gtt ctg ggc aag cag	480
Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln	
65 70 75 80	
gtg cta gtg gtg tgt ggt gtg gat gag gtc cag agc ccg gta gct gct	528
Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala	
85 90 95	
gta gag gcc ttc ctg atg gat gag ggc cgc tgg gag cgt cgg gcc acc	576
Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr	
100 105 110	
ctc cct caa gca gcc atg ggg gtt gca act gtg gag aga gat ggt atg	624
Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met	
115 120 125	
gtg tat gct ctg ggg gga atg ggc cct gac acg gcc ccc cag gcc cag	672
Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln	
130 135 140	
gta cgt gtg tat gac ccc cgt cgg gac tgc tgg ctt tcg cta ccc tcc	720
Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser	
145 150 155 160	
atg ccc aca ccc tgc tat ggg gcc tcc acc ttc ctg cac ggg aac aag	768
Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys	
165 170 175	
atc tat gtc ctg ggg ggc cgc cag ggc aag ctc ccg gtg act gct ttt	816
Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe	
180 185 190	
gaa gcc ttt gat ctg gag gcc cgt aca tgg acc cgg cat cca agc cta	864
Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu	
195 200 205	
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Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val	
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Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser	
225 230 235 240	
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Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly	
245 250 255	
tcc tgg acc aaa ttg ccc cgc agc ctg cgc atg agg gat aag agg gca	1056
Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala	
260 265 270	
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Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly	
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Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu	
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Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly	
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Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp  
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Gly Val

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ggc gtc agt ttc aaa ctg gaa gaa aaa acc gcc cac agc agc ctg gca 146  
Gly Val Ser Phe Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala  
30 35 40

ctc ttc aga gat gat acg ggt gtc aaa tat ggc ttg gtg gga ttg gag 194  
Leu Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu  
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ccc acc aag gtg gcc ttg aat gtg gag cgc ttc cgg gag tgg gca gtg 242  
Pro Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val  
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Val Leu Ala Asp Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val  
80 85 90

aca gtg aag cgc tcc cag cag ttc cgg ata gga gtg gca gat gtg gac 338  
Thr Val Lys Arg Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp  
95 100 105

atg tcc cgg gat agc tgc att ggt gtt gat gat cgt tcc tgg gtg ttc 386  
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acc tat gcc cag cgc aag tgg tac acc atg ttg gcc aac gag aaa gcc 434  
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Pro Val Glu Gly Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu  
145 150 155

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Ala Leu Trp Asp Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro				
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Glu Gly Leu				
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Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val				
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Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu				
40 45 50				
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Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile				
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Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Pro Ala Pro				
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Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala				
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Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met				
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Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly Phe				
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Val Ala Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala
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Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu
35          40          45
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Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn
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aca gta atg aaa gta aag cag atc ctg ggc aga agc tcc agt gat cca 303
Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro
65          70          75
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Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys
80          85          90
aat ggg aaa tta cga tat gaa ata gat act gga gaa gaa aca aaa ttt 399
Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe
95          100          105          110
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Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu
115          120          125
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Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr
130          135          140
gtc ccg ttt gat ttt gga gaa aag caa aaa aat gct ctt gga gaa gca 543
Val Pro Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala
145          150          155
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Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser
160          165          170
gca gct ctt ctt gct tat gga att gga caa gac tcc cct act gga aaa 639
Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys
175          180          185          190
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Ser Asn Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser
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Leu Ala Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn	
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Cys Gly Gly Ser Ser Arg Ile Pro Lys Leu Gln Gln Leu Ile Lys Asp	
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Ile Leu Val Lys Gly Val Asp Glu Ser Gly Ala Ser Arg Phe Thr Val	
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Val Leu Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp	
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Gln Glu Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser	
495 500 505	
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1747

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Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys  
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gag cac ttg gtc aac ata tct gga ggg ccc atg aca tac agc cac cgg 218  
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Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser  
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gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg 314  
Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg  
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gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca 362  
Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr  
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Met Ala Thr  
1  
cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg 165  
His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val  
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ggc aca gtg gct gtc act gtc atg cct cag tgg ata gtg tcg gcc ttc 213  
Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe  
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<213> Homo sapiens

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<222> 150..587

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<213> Homo sapiens

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                               Met Arg Leu Gln Asp
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Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
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cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg      402
His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
                90       95       100
gga gga gca cca ctg agg cct ggg gag tcg gaa cag ggc taaggagggg      451
Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu Gln Gly
                105       110
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aaa                                                                514
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<221> CDS

<222> 32..1132

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                               1       5
acc ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat      100
Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
                10       15       20
gcg gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc      148
Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
                25       30       35
gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc      196
Ala His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser
                40       45       50       55
ttc agc tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg      244
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tatgcacccg tgctgtggcg tgcccgtcgt ctgtgtggc atg cct gtc tgt gca 174  
Met Pro Val Cys Ala  
1 5  
ccc gtg ctg tgg cgt gcc cgt cgt ctg tgt ggc atg cct gtc tgt gca 222  
Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly Met Pro Val Cys Ala  
10 15 20  
ccc gtg ccg tgg cgt gcc cgt cgt ctg tgc acc cgt gct gtg gtg tgc 270  
Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr Arg Ala Val Val Cys  
25 30 35  
cct tcg tct gtt cct ttt att gcc ggg cag ggt tgc acc cac atg tgc 318  
Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly Cys Thr His Met Cys  
40 45 50  
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Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser Pro Leu Ala Gly Gly  
55 60 65  
gtg atc ctg ggt gtg gcc ctg tgg ctc cgc cat gac ccg cag acc acc 414  
Val Ile Leu Gly Val Ala Leu Trp Leu Arg His Asp Pro Gln Thr Thr  
70 75 80 85  
aac ctc ctg tat ctg gag ctg gga gac aag ccc gcg ccc aac acc ttc 462  
Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe  
90 95 100  
tat gta ggc atc tac atc ctc atc gct gtg ggc gct gtc atg atg ttc 510  
Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly Ala Val Met Met Phe  
105 110 115  
gtt ggc ttc ctg ggc tgc tac ggg gcc atc cag gaa tcc cag tgc ctg 558  
Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu  
120 125 130  
ctg ggg acg ttc ttc act tgc ctg gtc atc ctg ttt gcc tgt gag gtg 606  
Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu Phe Ala Cys Glu Val  
135 140 145  
gcc gcc ggc atc tgg ggc ttt gtc aac aag gac cag atc gcc aag gat 654  
Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp Gln Ile Ala Lys Asp  
150 155 160 165  
gtg aag cag ttc tat gac cag gcc cta cag cag gcc gtg gtg gat gat 702  
Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp  
170 175 180  
gac gcc aac aac gcc aag gct gtg gtg aag acc ttc cac gag acg ctt 750  
Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe His Glu Thr Leu  
185 190 195  
gac tgc tgt ggc tcc agc aca ctg act gct ttg acc acc tca gtg ctc 798  
Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr Thr Ser Val Leu  
200 205 210  
aag aac aat ttg tgt ccc tcg ggc agc aac atc atc agc aac ctc ttc 846

Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe  
 215 220 225  
 aag gag gac tgc cac cag aag atc gat gac ctc ttc tcc ggg aag ctg 894  
 Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu  
 230 235 240 245  
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 Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala Val Ile Met Ile Phe  
 250 255 260  
 gag atg atc ctg agc atg gtg ctg tgc tgt ggc atc cgg aac agc tcc 990  
 Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly Ile Arg Asn Ser Ser  
 265 270 275  
 gtg tac tgaggccccg cagctctggc cacagggacc tctgcagtgc cccctaagtg 1046  
 Val Tyr  
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 ccaccacagcc cgcccgctcct gtgggctgca cagctcacct tgttccctcc tgccccggtt 1406  
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 ctg ctg gtg aaa cgg ctg cag gag gtg agc tcc cgg gat ggg aaa ggc 97  
 Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly  
 15 20 25  
 gac ctg ggg gag ccg ccc ccg aca cgg ccc acg gtg ggc acc aat ctt 145  
 Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu  
 30 35 40 45  
 act gac atc gtg gca cag aga aag atc acc atc cgg gag ctt ggg ggg 193  
 Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly  
 50 55 60  
 tgc atg ggc ccc atc tgg tcc agt tac tat gga aac tgc cgt tct ctc 241  
 Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu  
 65 70 75  
 ctg ttt gtg atg gac gcc tct gac ccc acc cag ctc tct gca tcc tgt 289  
 Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys  
 80 85 90  
 gtg cag ctc tta ggt ctc ctt tct gca gaa caa ctt gca gaa gca tcg 337  
 Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser  
 95 100 105  
 gtg ctg ata ctc ttc aat aaa atc gac cta ccc tgt tac atg tcc acg 385  
 Val Leu Ile Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr  
 110 115 120 125  
 gag gag atg aag tca tta atc agg ctt cca gac atc att gct tgt gcc 433

Glu	Glu	Met	Lys	Ser	Leu	Ile	Arg	Leu	Pro	Asp	Ile	Ile	Ala	Cys	Ala		
				130					135					140			
aag	cag	aac	atc	acc	acg	gca	gaa	atc	agc	gcc	cgt	gaa	ggc	act	ggc		481
Lys	Gln	Asn	Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly		
			145					150					155				
tta	gca	ggg	gtg	ctg	gcc	tgg	ctc	cag	gcc	acc	cac	aga	gcc	aac	gat		529
Leu	Ala	Gly	Val	Leu	Ala	Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp		
		160					165						170				
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gctttgctgc	caatagtttc	ttctcacagg	ggcagaataa	cccaaagtaa	ccctacatga												649
tggggctctg	tgctgggatg	caatgatgtg	taaactgagg	catgtggaga	tggaagttga												709
catctggcct	ctgaaaaaag	tgtccccagg	ggctaggcat	ggtggctcac	acctgtaac												769
ccagcacttt	gagaggccga	ggcgggtgta	tcacctgagg	tcgggagttc	gagactagcc												829
tgaccaacat	ggagaaaccc	tgtctctact	aaaaatacaa	aattagctgg	gtgtgctggt												889
gcatgcctgt	aatctcagct	acttgggagg	ctgagacagg	agaatccctt	gaacctggga												949
ggtggagggt	gcagtgaagc	gagatcatgc	cattgcactg	cacctgggca	acaagagtga												1009
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gcaccttccg	gaaa	atg	gcg	gct	gcc	agg	ccc	agc	ctg	ggc	mga	gtc	ctc				170
	Met	Ala	Ala	Ala	Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu					
	1				5					10							
cca	gga	tcc	tct	gtc	ctg	ttc	ctg	tgt	gac	atg	cag	gag	aag	ttc	cgc		218
Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu	Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg		
	15				20					25							
cac	aac	atc	gcc	tac	ttc	cca	cag	atc	gtc	tca	gtg	gct	gcc	cgc	atg		266
His	Asn	Ile	Ala	Tyr	Phe	Pro	Gln	Ile	Val	Ser	Val	Ala	Ala	Arg	Met		
	30				35					40							
ctc	aag	gtg	gcc	cgg	ctg	ctt	gag	gtg	cca	gtc	atg	ctg	acg	gag	cag		314
Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu	Val	Pro	Val	Met	Leu	Thr	Glu	Gln		
	45			50				55						60			
tac	cca	caa	ggc	ctg	ggc	ccc	acg	gtg	ccc	gag	ctg	ggg	act	gag	ggc		362
Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr	Val	Pro	Glu	Leu	Gly	Thr	Glu	Gly		
		65			70					75							
ctt	cgg	ccg	ctg	gcc	aag	acc	tgc	ttc	agc	atg	gtg	cct	gcc	ctg	cag		410
Leu	Arg	Pro	Leu	Ala	Lys	Thr	Cys	Phe	Ser	Met	Val	Pro	Ala	Leu	Gln		
		80				85				90							
cag	gag	ctg	gac	agt	cgg	ccc	cag	ctg	cgc	tct	gtg	ctg	ctc	tgt	ggc		458
Gln	Glu	Leu	Asp	Ser	Arg	Pro	Gln	Leu	Arg	Ser	Val	Leu	Leu	Cys	Gly		
	95				100					105							
att	gag	gca	cag	gcc	tgc	atc	ttg	aac	acg	acc	ctg	gac	ctc	cta	gac		506
Ile	Glu	Ala	Gln	Ala	Cys	Ile	Leu	Asn	Thr	Thr	Leu	Asp	Leu	Leu	Asp		
	110				115					120							
cgg	ggg	ctg	cag	gtc	cat	gtg	gtg	gac	gcc	tgc	tcc	tca	cgc	agc			554
Arg	Gly	Leu	Gln	Val	His	Val	Val	Val	Asp	Ala	Cys	Ser	Ser	Arg	Ser		
	125			130					135					140			
cag	gtg	gac	cgt	ctg	gtg	gct	ctg	gcc	cgc	atg	aga	cag	agt	ggt	gcc		602

Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala  
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Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala  
160 165 170  
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc 698  
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala  
175 180 185  
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc 746  
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu  
190 195 200  
cac tgaactccaa ccctgccttg agggaagacc accctcctgt caccocggacc 799  
His  
205  
tcagtggaag cccgttcccc ccattccctgg atcccaagag tgggtgcgac caccaggagt 859  
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tcggccccgg gccacttcac ggggcgggaa ggggagggga agaagagtct cagactgtgg 1039  
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Met Trp Leu Tyr Arg Asn  
1 5  
ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att 163  
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile  
10 15 20  
gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag 211  
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys  
25 30 35  
aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt 259  
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu  
40 45 50  
gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta 307  
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val  
55 60 65 70  
ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta 355  
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu  
75 80 85  
gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag 403  
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu  
90 95 100  
ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt 451  
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly  
105 110 115  
ctg gcc ttt gcg tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca 499  
Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr  
120 125 130



aaa taaacagctt gcacttgaaa aaaaaaaaaa aaa

703

Lys

150

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<211> 849

<212> DNA

<213> Homo sapiens

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<222> 165..674

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tgcaagcgcg cgtgggaggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg 120  
atgtttcccg ggaagaactg ggataaagga aggtcccag cacc atg gag gac ccg 176  
Met Glu Asp Pro

1

aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224  
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser  
5 10 15 20

ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc 272  
Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys  
25 30 35

acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac 320  
Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His  
40 45 50

atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg 368  
Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly  
55 60 65

gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa 416  
Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys  
70 75 80

gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc 464  
Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr  
85 90 95 100

ctg ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac 512  
Leu Pro Val Ala Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp  
105 110 115

tgt ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag 560  
Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln  
120 125 130

atg cat gag gtc cgt gcc cct cct gcc acc ttc gcc tgc aca gag tgc 608  
Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys  
135 140 145

ggc cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg 656  
Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg  
150 155 160

cat gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacgggtgac 704  
His Ala Arg Gly Glu Leu  
165 170

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<400> 162

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Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala Ala
10               15               20               25
aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc cat      150
Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala His
               30               35               40
tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc agc      198
Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser
               45               50               55
tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg tgc gag      246
Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu
               60               65               70
gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc tgg ttc      294
Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe
               75               80               85
atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac cgc gac      342
Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp
90               95               100               105
aac atc atc agt gac tat gac cag atc att gac tat gtg gag cgc acc      390
Asn Ile Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu Arg Thr
               110               115               120
ttc aca gga gag cac gtg gtg gcc ctg atg ccc gag gtg ggc agc ctg      438
Phe Thr Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly Ser Leu
               125               130               135
cag cac gca cgg gtg ctg cag tac cgg gag ctg ctg gac gca ctg ccc      486
Gln His Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala Leu Pro
               140               145               150
atg gat gcc tac acg cat ggc tgc atc ctg cat ctc gag ctc acc acc      534
Met Asp Ala Tyr Thr His Gly Cys Ile Leu His Leu Glu Leu Thr Thr
155               160               165
gac tcc atg atc ccc aag tac gcc acg gcc gag atc cgc aga cat tta      582
Asp Ser Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg His Leu
170               175               180               185
gcc aat gcc acc acg gac ctc atg aaa ctg gac cat gaa gag gag ccc      630
Ala Asn Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu Glu Pro
               190               195               200
cag ctc tcc gag ccc tac ctt tct aaa caa aag aag ctc atg gcc aag      678
Gln Leu Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met Ala Lys
               205               210               215
atc ttg gag cat gat gat gtg agc tac ctg aag aag atc ctc ggg gaa      726
Ile Leu Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu
               220               225               230
ctg gcc atg gtg ctg gac cag att gag gcg gag ctg gag aag agg aag      774
Leu Ala Met Val Leu Asp Gln Ile Glu Ala Glu Leu Glu Lys Arg Lys
235               240               245
ctg gag aac gag ggg cag aaa tgc gag ctg tgg ctc tgt ggc tgt gcc      822
Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Ala
250               255               260               265
ttc acc ctc gct gat gtc ctc ctg gga gcc acc ctg cac cgc ctc aag      870
Phe Thr Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys
               270               275               280
ttc ctg gga ctg tcc aag aaa tac tgg gaa gat ggc agc cgg ccc aac      918
Phe Leu Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn

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285	290	295	
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300	305	310	
gtc ctg ggt gac atc cac acc acc ctg ctg tcg gcc gtc atc ccc aat			1014
Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn			
315	320	325	
gct ttc cgg ctg gtc aag agg aaa ccc cca tcc ttc ttc ggg gcg tcc			1062
Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser			
330	335	340	345
ttc ctc atg ggc tcc ctg ggt ggg atg ggc tac ttt gcc tac tgg tac			1110
Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr			
350	355	360	
ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac			1158
Leu Lys Lys Lys Tyr Ile			
365			
aaaaaamaaa aaaaaaaa			1176

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 <213> Homo sapiens

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gcaccttccg gaaa atg gcg gct gcc agg ccc agc ctg ggc cga gtc ctc	170
Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu	
1 5 10	
cca gga tcc tct cct gtt cct gtg tgacatgcag gagaagtcc gccacaacat	224
Pro Gly Ser Ser Pro Val Pro Val	
15 20	
cgctacttcc ccacagatcg tctcagtggc tgcccgcgat ctcaaggtgg cccggtgct	284
tgaggtgcca gtcagtctga cggagcagta cccacaaggc ctgggccccg cgtgcccga	344
gctgggggact gagggccttc ggccgctggc caagacctgc ttcagcatgg tgcttgcct	404
gcagcaggag ctggacagtc ggccccagct gcgctctgtg ctgctctgtg gcattgaggc	464
acaggcctgc atcttgaaca cgacctgga cctcctagac cgggggctgc aggtccatgt	524
ggtggtggac gcctgtcct caccagcca ggtggaccgg ctggtggctc tggcccgcat	584
gagacagagt ggtgccttcc tctccaccag cgaagggtc attctgcagc ttgtgggcga	644
tgccgtccac cccagttca aggagatcca gaaactcatc aaggagcccg cccagacag	704
cggactgctg ggctcttcc aaggccagaa ctccctctc cactgaactc caaccctgcc	764
ttgagggaag accaccctcc tgtcaccgg acctcagtgg aagcccgttc ccccatccc	824
tgatcccaa gagtgggtgc atccaccagg agtgccggcc ccttgggggg ggcagggtgc	884
tgcttccca ttggacagct gctcccgaa atgcaaatga gactcctgga aactgggtgg	944
gaattggctg agccaagatg gagggggggc tcggccccgg gccacttcac ggggcgggaa	1004
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ggcaaaaaaa aaaaaaaaaa	1084

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<221> CDS

<222> 173..847

<400> 164

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gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca      178
                                         Met Ala
                                         1
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
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gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc      274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
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ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu
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tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc      370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile
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tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga      418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly
          70                      75                      80
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc      466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala
          85                      90                      95
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg      514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val
          100                     105                     110
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc      562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly
          115                     120                     125                     130
atg gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga      610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg
          135                     140                     145
gat ttc tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga      658
Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
          150                     155                     160
gaa gct ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga      706
Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly
          165                     170                     175
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc      754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser
          180                     185                     190
tac aga tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac      802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
          195                     200                     205                     210
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg      847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
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acttttctcaa aatggacccc aaagaaaactt tgatttactg ttcttaactg cctaattctta      967
attacaggaa ctgtgcatca gctattttatg atttctataag ctatttcagc agaatgagat      1027
attaaaccca atgcttttgat tgttctagaa agtattgttaa tttgttttct aaggtgggtc      1087
aagcatctac tcttttttato atttacttca aaatgacatt gctaaagact gcattattct      1147
actactgtaa tttctccacg acatagcatt atgtacatag atgagtgtaa catttatatc      1207
tcacatagag acatgcttat atgggttttat ttaaaatgaa atgccagtcc attacactga      1267
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ataaatagaa ctcaactatt gcttttcagg gaaatcatgg atagggttga agaaggttac 1327
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 <212> DNA  
 <213> Homo sapiens

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 <222> 8..1141

<220>  
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 <222> 1707  
 <223> n=a, g, c or t

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tac cag gat ttc tat gca ttc gac ctg tca gga gcc act cga gtc ctt 97
Tyr Gln Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu
15          20          25          30
gaa tgg att gat gac aaa gga gtc ttt gtt gct ggc tat gaa agc ctg 145
Glu Trp Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu
      35          40          45
aaa aag aat gaa att ctt cat ctg aaa tta cct ctc aga ctt tct gta 193
Lys Lys Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val
      50          55          60
aag gaa aac aag ggc tta ttc cca gaa aga gat ttc aaa gtg cgc cat 241
Lys Glu Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His
      65          70          75
gga gga ttt tca gac agg tct atc ttt gat cta aag cat gtg cca cat 289
Gly Gly Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His
      80          85          90
acc aga ttg ctg gtt acc agt ggc ctt cca ggt tgt tat ctg cag gtg 337
Thr Arg Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val
95          100          105          110
tgg cag gtt gca gag gac agt gat gtc att aaa gct gtc agc acc att 385
Trp Gln Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile
      115          120          125
gct gtg cat gag aaa gag gag agt ctc tgg cct agg gtg gcc gtc ttc 433
Ala Val His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe
      130          135          140
tcc aca ttg gca ccc gga gtc ctc cat ggg gcg agg ctc cga agt ctg 481
Ser Thr Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu
      145          150          155
cag gtc gtt gat ctg gag tcc cgg aag acc acg tac acc tca gat gtc 529
Gln Val Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val
      160          165          170

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agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc	577
Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr	
175 180 185 190	
ttt gcc ttc tgc tgt gct tgc ggc cgg ctg ggg ctt gtt gac acc cgg	625
Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg	
195 200 205	
cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt	673
Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly	
210 215 220	
gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg	721
Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly	
225 230 235	
ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac	769
Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp	
240 245 250	
ccc cgg gat ctg tgc cat cct gtg agc tca gtc cag tgc cca gta tcc	817
Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser	
255 260 265 270	
gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc	865
Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly	
275 280 285	
ctg aag aat tgc ttg gcc atc tca ggt ttt gat ggt aca gtc cag gtc	913
Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val	
290 295 300	
tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg	961
Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg	
305 310 315	
agc caa gta gaa cct ctg ttc act cac aga ggt cac atc ttc cta gat	1009
Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp	
320 325 330	
gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat	1057
Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His	
335 340 345 350	
ccc tgc aga cca agg act ttg tta tca gca aca aat gat gcc tct ctg	1105
Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu	
355 360 365	
cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc	1151
His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg	
370 375	
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taggactcaa gtgactacca gtccctgtta ccagctgtgt ggccttgggc aagtctgcc	1271
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gcccatagtg aatatntaaa gtgtgctgga catgggtggct catgcctgta atcccagcac	1751
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<212> DNA

<213> Homo sapiens

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 tcatcccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt 171  
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe  
 1 5 10  
 ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct 219  
 Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro  
 15 20 25  
 cag tgg aga gtg tgc gcc ttc att gaa aac aac atc gtg gtt ttt 264  
 Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe  
 30 35 40  
 taaaacttct gggaaggact gtggatgaat tgcgtgaggc aggctaacat caggatgcag 324  
 tgcaaaatct atgattccct gctggctcct tctccggacc tacaggcagc cagaggactg 384  
 atgtgtgctg cttccgtgat gtccttcttg gctttcatga tggccatcct tggcatgaaa 444  
 tgcaccaggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga 504  
 atcatcttca tcatcacggg catggtgggt ctcatccctg tgagctgggt tgccaatgcc 564  
 atcatcagag atttctataa ctcaatagtg aatgttgccc aaaaacgtga gcttggagaa 624  
 gctctctact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc 684  
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 tatgtgtagt tgtgtatggt tttttaactt tactataaag ccatgcaaat gacaaaaatc 864  
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 atcttaatta caggaactgt gcatcagcta tttatgattc tataagctat ttcagcagaa 984  
 tgagatatta aaccgaatgc tttgattggt ctagaaagta tagtaatttg ttttctaagg 1044  
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 cactgaataa atagaactca actattgctt ttcagggaaa tcatggatag ggttgaagaa 1284  
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 tcaaactgct tttccagggc tatactcaga agaaagataa aagtgtgatc taagaaaaag 1584  
 tgatgggtttt aggaagtga aaatatcttt gtttttgtat ttgaagaaga atgatgcatt 1644  
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 <212> DNA  
 <213> Homo sapiens

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 tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag 97  
 Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu  
 15 20 25  
 ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac 145

Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn		
30						35					40						
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193	
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val		
45					50					55					60		
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggt	gaa	gca	tac	aag	aga	241	
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg		
				65					70					75			
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289	
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro		
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Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe		
		95					100					105					
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg	385	
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu		
	110					115					120						
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggt	ata	aaa	gct	gat	tgg	ttg	433	
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu		
	125				130						135				140		
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481	
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn		
				145					150					155			
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggg	att	529	
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile		
			160					165					170				
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577	
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu		
		175					180					185					
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625	
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val		
			190			195					200						
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673	
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe		
	205				210					215					220		
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721	
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile		
				225					230					235			
gtg	aac	att	ctg	ggg	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769	
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala		
			240				245						250				
ggg	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggg	aaa	gtt	gcc	aca	gga	817	
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly		
		255				260						265					
aga	tat	gga	cca	tca	ctt	ggg	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865	
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met		
		270				275					280						
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913	
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala		
				285		290				295					300		
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggg	cat	961	
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His		
				305				310						315			
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa	1009	
Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu		
			320					325					330				
ata	agg	act	aat	ggc	ccc	aaa	aaa	gga	ggg	ggc	tct	aag	taaaaactggg			1058	
Ile	Arg	Thr	Asn	Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys					

335	340	345	
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gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc	1178		
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 <222> 70..777

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Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser	
1 5 10	
tcg gtg gca ggg cct gac tgc tgc gga ggc ctc ggc aat att gat ttt	159
Ser Val Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe	
15 20 25 30	
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Arg Gln Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp	
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ccc ctg gat ccc agc ttt gtg gct gcc gtc atc acc atc acc ttc aat	255
Pro Leu Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn	
50 55 60	
ccg ctc tac tgg aat gtg gtt gca cga tgg gaa cac aag acc cgc aag	303
Pro Leu Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys	
65 70 75	
ctg agc agg gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc	351
Leu Ser Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser	
80 85 90	
atc acc atc ctg ctc ctg aac ttc ctg cgc tgc cac tgc ttc acg cag	399
Ile Thr Ile Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln	
95 100 105 110	
gcc atg ctg agc cag ccc agg atg gag agc ctg gac acc ccc gcg gcc	447
Ala Met Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala	
115 120 125	
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Tyr Ser Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu	
130 135 140	
tcc agc ttc ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac	543
Ser Ser Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr	
145 150 155	
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Phe Gly Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile	
160 165 170	
ctg gac aac ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg	639
Leu Asp Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp	
175 180 185 190	
gcc atc atg cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg	687
Ala Ile Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val	
195 200 205	
gcc ctc acc tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct	735
Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala	

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Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg				
	10 15 20			
caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat				151
Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn				
	25 30 35			
tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg				199
Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu				
	40 45 50			
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Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala				
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Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His				
	75 80 85			
cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg				343
Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met				
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Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val				
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Ile Thr Ile				
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 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
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 gag ggc cgg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
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 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu  
 100 105 110  
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443  
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile  
 115 120 125  
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 Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr  
 130 135 140  
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539  
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro  
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 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 160 165 170  
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 caccccaatg ggaccaccct cctgggtccc ctgggtgccg ttttccttag aaatcagaga 712  
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tggctacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt      174
                               Met Leu Ser Lys Gly
                               1           5

ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc      222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val
                               10           20

gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc      270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro
                               25           30           35

ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc      318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu
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cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg      366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu
                               55           60           65

gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct      414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala
70           75           80           85

gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac      462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp
                               90           95           100

aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc      510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser
                               105           110           115

ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa      558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln
120           125           130

ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg      606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala
135           140           145

ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta      654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu
150           155           160           165

ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg      702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met
170           175           180

tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc      750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly
185           190           195

cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc      798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala
200           205           210

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Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu
215           220           225

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Arg Pro Pro Gly Pro Gly Arg
230           235

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agtacagaga acagggcttg ggccactttg gagagacaga atctagtcct gggcaacttc      1017
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           Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu  
           1                  5                  10  
 ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat 157  
 Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp  
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 Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn  
                   35                  40                  45  
 aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt 253  
 Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val  
                   50                  55                  60  
 ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca 301  
 Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser  
           65                  70                  75  
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 Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser  
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 gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg 397  
 Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu  
           95                  100                  105                  110  
 gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att 445  
 Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile  
                   115                  120                  125  
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 Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu  
                   130                  135                  140  
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 Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly  
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 Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln  
           160                  165                  170  
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	Met Ala Glu Pro Asp	Pro Ser His	Pro Leu Glu Thr Gln												
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Ala Gly Lys Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly															
15	20	25													
gga gcc gct ggt gga gaa gca gac atg gac ttc ctg cgg aac tta ttc	266														
Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe															
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Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg															
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	80	85	90												
ccc gac ttt cgc tct cca tcc acc ggc ctc tat gac aac cta gag aag	458														
Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys															
	95	100	105												
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Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys															
	110	115	120	125											
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Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly															
	130	135	140												
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Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu															
	160	165	170												
cga ata gcc ggg ctg gaa cag gag gac ttg gtg gag gcg cac ggc acc	698														
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	175	180	185												
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Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro															
	190	195	200	205											



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Ser Arg Ala Ser Trp	Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly					
	15	20	25			
cac acg gac aaa caa cag aca gaa gac gta ctg gcc gct gga ctc cgc	387					
His Thr Asp Lys Gln Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg						
	30	35	40			
tgc ctc ccc cat ctc ccc gcc atc tgc gcc cgg agg atg agc cca gcc	435					
Cys Leu Pro His Leu Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala						
	45	50	55			
ttc agg gcc atg gat gtg gag ccc cgc gca aaa ggc gtc ctt ctg gag	483					
Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu						
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Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg Phe Asn						
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Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly						
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Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile Val Asp						
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Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu						
	205	210	215			
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Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser						
	220	225	230	235		
atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat gca aag	1011					
Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys						
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Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu	
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Lys Leu Leu	Ala Glu Met	Lys Met	Lys Lys	Asp Leu	Phe Pro Val Gly	
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Pro Gly Lys	Ser Val Leu	Ile Met	Asp Gly	Ala Ser	Ala Phe Gly Thr	
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Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe
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Leu Pro Ser Cys Trp Asp Gln Ser Phe Leu Thr Asn Ile Thr Phe Leu			
90 95 100			
aag gtt ctt ctc tgg ttg gtc ctg ctg gga ctg ttt gtg gaa ctg gaa			388



tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat	196
Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp	
45 50 55	
ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac	244
Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr	
60 65 70	
ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc	292
Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala	
75 80 85 90	
agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg	340
Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Ser Ala His Phe Leu	
95 100 105	
ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg	388
Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr	
110 115 120	
ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc	436
Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile	
125 130 135	
gcg gcc ttc acc agg tagctacgga caccgggat accccacact gggggccctcc	491
Ala Ala Phe Thr Arg	
140	
tcctgggcct gaccagtccc ccagctgtca cctccccatt cctggacagg aagggcactt	551
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ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc	1391
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ccaaaactta caggcttaaa acaacaaaca tgtatcattt cttatgattc tgtgggttgg	180
ctgggtggtt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct	237
Met Ser	
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ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg	285
Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu Pro Val	
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207

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aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg      1159
Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
      120              125              130
ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag      1213
Leu Met Pro Val Ile Pro Ala Phe
135              140
gtcagggtgtt cgagaccagc ctggccaacg tggtgaaacc tcgtctctac taaaaaatac      1273
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caagagaata acttgaaccc aggaggcgga ggggtgcagtg agctgagatc ctgccgctgc      1393
actccagcct ggggtgacaga gcacactccg tctcaaaaaa ggaaagctga tgagaaattg      1453
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tcaaaagaac acaggaagtg atttgctact tgaaagaaag gcaaccctc cccaaggaag      1633
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gcctcggcct cccaaagtgc tgggggttaca ggcattagacc accgcacccg gcccccttcc      240
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aacacttcat catccaccac ctctctggagg gggtagcccg aggtgctccg ctggggactc      360
tgctcattct ggggggtgcag ttgacgggtg gtcgtgatct ttcccgtaat ctgtcccctc      420
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agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca      530
Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
      1      5      10      15
gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt      578
Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
      20      25      30
ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat      626
Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
      35      40      45
gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct      674
Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
      50      55      60
gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt      722
Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
      65      70      75
ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc      770
Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
      80      85      90      95
ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
      100      105      110

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gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc 866  
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val  
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cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc 914  
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser  
130 135 140  
aga aac gat gaa acc tta taagagtga attatcatgt gcaagagtga 962  
Arg Asn Asp Glu Thr Leu  
145  
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag 1022  
cactcagttt tggcagagct ttttctgccc aatgtttact cacattcact gtccgagatt 1082  
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Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys  
1 5 10  
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg 160  
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu  
15 20 25  
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc 208  
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly  
30 35 40  
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg 256  
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu  
45 50 55  
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac 304  
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His  
60 65 70 75  
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt 364  
gtcctgtttc ccccttttta attttatccc ttgctagaat taagatacta tatgcctcac 424  
ttatcaatta cagtctaaat ccaaaagaaa aaaaaaaaaa 463  
  
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 aaaggactct ggattgggtg gcagtctgct ttttttttc caaggatgatc actttactgt 180  
 agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229  
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys  
 1 5 10  
 ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277  
 Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln  
 15 20 25 30  
 cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325  
 Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp  
 35 40 45  
 aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373  
 Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr  
 50 55 60  
 tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421  
 Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr  
 65 70 75  
 gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469  
 Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr  
 80 85 90  
 cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517  
 Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His  
 95 100 105 110  
 tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565  
 Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His  
 115 120 125  
 ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613  
 Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr  
 130 135 140  
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 Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu  
 145 150 155  
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 Phe Ile Ile Val Phe Ile Leu Ile Phe Phe  
 160 165  
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 aa 773

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 Met Pro Arg Ser Ser Arg Ser  
 1 5

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cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
      10      15      20
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag      210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
      25      30      35
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
      40      45      50      55
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
      60      65      70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
      75      80      85
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg      402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp
      90      95      100
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga      450
Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly
      105      110      115
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat      498
Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His
      120      125      130      135
tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca      546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro
      140      145      150
ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca      593
Gly Gly Gly Ile Pro Gly Pro Trp His
      155      160
agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga      653
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<222> 181..462

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attgagttat tacatatcaa ttgaacaagg tagttttaaa atgaaagaaa atcttgcaac      180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc      228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
      1      5      10      15
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct      276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
      20      25      30
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga      324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg
      35      40      45
ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg      372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro

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tcc gcc ctc cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg			420
Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg			
65	70	75	80
agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc			462
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser			
85	90		
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca			522
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Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala	
20 25 30	
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc	146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu	
35 40 45	
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc	194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser	
50 55 60	
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca	242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr	
65 70 75	
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat	290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp	
80 85 90 95	
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gtggcgggcg ccctgtagtc ccagctactc gggaggctga nggcaggaga atggtgtgaa	890
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 Met  
 1  
 aaa aaa aag gaa gaa aca aca ctt tca gag atg gag cct gtt gag cca 165  
 Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu Pro  
 5 10 15  
 cag tac caa cta gtc aat gct gaa tcg act tct ccc ttt cta cat tgc 213  
 Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His Cys  
 20 25 30  
 ctg aga gaa gtc att ggg gaa tac tct gta cac gaa ttt tca ctg ttg 261  
 Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu Leu  
 35 40 45  
 ggg aaa aca gag agt caa ggg att gga ttg tgg att gca ttg gtg gtt 309  
 Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val Val  
 50 55 60 65  
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 Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn Ala  
 70 75 80  
 gag cag ccc ttc ttc aaa gaa cct cct acg gaa gct gct aag gaa ctc 405  
 Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu Leu  
 85 90 95  
 agt ctg tagctctgcg tggagccatg tgtaaact gaactgagac ctgccacctc 461  
 Ser Leu  
 ctactaccta agggcccatt ttcattctgat atcatccccc agaaacaaac tcatgatgac 521  
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 ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac 95  
 Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp  
 20 25 30  
 cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag 143  
 Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys  
 35 40 45

gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tcg gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	
gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcagagtca gcagggggccg	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgccccgg ccagaacggg cagggctgcc actgacctga agactccgga ctgggacccc	448
actccgaggg cagctcccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa	508
ataaaaaaaaa aaaaaaaaa	526

<210> 191  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 174..527

<400> 191	
attttcctgt taggccaaga gagaagagga tccttctctca gagcctccag cctcccttga	60
tcccttgctt gtgggcatat gtgggtcata tttccctccc atcaccctct gcacgccacc	120
cccatcaccg ccacagaccc ccagcccttc agttgccttg cacctccttg gtg atg	176
Met	
1	
cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
5 10 15	
tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
20 25 30	
tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
35 40 45	
ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa	368
Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
50 55 60 65	
aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga	416
Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
70 75 80	
gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt	464
Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
85 90 95	
gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
100 105 110	
agg act tcc tcc ctc taaggagctc cccatacccc ccatcacctt ggcattccca	567
Arg Thr Ser Ser Leu	
115	

gctcctccag	aatccctccc	tccctcagcc	tagagaagga	caactgcttc	cccttggggc	627
ttgtcccctc	acctccttga	ggaaagaact	gggagtaa	ctgcttgaag	ttctcctcat	687
tgacaattcc	gctgggacat	tcctggaagg	agagggcacc	aggctgaggg	cagagacaaa	747
atcccccttc	gttcaccgcc	cccaccctcc	atggcccaag	actcccaggg	agggggataa	807
tcttcaagcc	tccagaggac	tcaccacgtg	gctcatgtga	tgggagggaa	gacttctttc	867
ccagtgcaca	aataaaaaac	atggaacgaa	aaaaaaaaaa	aaa		910

<210> 192  
 <211> 668  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 57..203

<400> 192																
tcctgtcgac	gtgttcttcc	ggtagggcggag	cggcggatta	gccttcgcgg	ggcaaa	atg									59	
						Met										
						1										
gag	ctc	gag	gcc	atg	agc	aga	tat	acc	agc	cca	gtg	aac	cca	cct	gtc	107
Glu	Leu	Glu	Ala	Met	Ser	Arg	Tyr	Thr	Ser	Pro	Val	Asn	Pro	Pro	Val	
			5					10					15			
ttc	ccc	cat	ctg	acc	gtg	gtg	ctt	ttg	gcc	att	ggc	atg	ttc	ttc	acc	155
Phe	Pro	His	Leu	Thr	Val	Val	Leu	Leu	Ala	Ile	Gly	Met	Phe	Phe	Thr	
		20				25					30					
gcc	tgg	ttc	ttc	gtg	tat	cct	ttc	act	gag	cag	cca	gag	gac	cag	cat	203
Ala	Trp	Phe	Phe	Val	Tyr	Pro	Phe	Thr	Glu	Gln	Pro	Glu	Asp	Gln	His	
	35					40				45						
tagtgatgtg	ggaagctcag	ggagaaacca	cgctaggtac	atggaccccg	ccggttttgt											263
acattggatt	ggggctgaga	gaagattgcc	gtgggctggg	ctctctgcac	tccacagtcc											323
acccttctgc	tttgcttaaa	ctgctgtgcc	cagttacgag	gtcacctcta	ccaagtacac											383
tcgtgatatc	tataaagagc	tcctcatctc	attagtggcc	tcactcttca	tgggcttttg											443
agtcctcttc	ctgctgtctc	gggttggcat	ctacgtgtga	gcacccaagg	gtaacaacca											503
gatggcttca	ctgaaacctg	ctttttgtaa	ttactttttt	ttactgttgc	tgggaagtgc											563
ccacctgctg	ctcataataa	atgcagatgt	atagcaaaaa	aaaaaaaaaa	aaaaaaaaaa											623
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaa												668

<210> 193  
 <211> 637  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 68..334

<400> 193																
agttatgaag	ttctaaaagc	aagtcttaat	caggaagtgt	ccttgatcac	caacggctcg											60
cccaggc	atg	ctg	gct	ctc	ttc	cac	ttc	cac	ctt	cca	cca	tgg	gat	gac		109
	Met	Leu	Ala	Leu	Phe	His	Phe	His	Leu	Pro	Pro	Trp	Asp	Asp		
	1				5					10						
gca	gta	aga	agg	cca	tca	gta	gat	gcc	agt	ccc	tca	acc	ttg	aac	ttt	157
Ala	Val	Arg	Arg	Pro	Ser	Val	Asp	Ala	Ser	Pro	Ser	Thr	Leu	Asn	Phe	
	15				20				25				30			
cca	gac	gca	gaa	ctt	tat	gcc	tcc	att	ttc	ctc	tgc	tgc	atg	gcc	cca	205
Pro	Asp	Ala	Glu	Leu	Tyr	Ala	Ser	Ile	Phe	Leu	Cys	Cys	Met	Ala	Pro	
		35						40					45			

gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca	253
Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala	
50 55 60	
aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc	301
Asn Gly Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val	
65 70 75	
tgg cat gaa aat tca caa gaa gag agg aaa tac tgaggagaaa atggcagatt	354
Trp His Glu Asn Ser Gln Glu Glu Arg Lys Tyr	
80 85	
gtgtttgctg aatttgattg acgaagaagt caccatgaaa atcacagtga accatttgga	414
aagcaaactg ccaaaaaaat aatagttagt catgctctca ggctggttgt tttggctggt	474
gtgggtttct tgcatttcca gatgattgca aagagctggt tctcaatttc tgcaacaagt	534
gccagctgaa attttggtac cagtttcatt aaatatgtat aacaaaaaaa aaaaaaaaaa	594
aaaaaaaaaa aaaaaaaaaa aaaaaaagaa aaaaaaaaaa aaa	637

<210> 194  
 <211> 706  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 183..443

<400> 194	
agaagttctc agaggggtgag ggtcccacat ctctgcagg acaggcccta gctaccgagt	60
cacagaaacc cagggccgaa gcaaagtccc aatcccagag aggctggggc acacctacaa	120
ctgaaaggag gcttagaaat ctttcagaga ccaccctatc ggttctcctc cacctggaca	180
gg atg agc cag caa cac aga agg aag agg cct tcc tcc gaa aga aaa	227
Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys	
1 5 10 15	
agc aca aga aag atg gac aca tgg cag agt ctt aaa gtc aaa gaa gta	275
Ser Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val	
20 25 30	
ttc tgt aag cat aat tct tcc tat gaa tgc ctt ctc tat aaa gag gtt	323
Phe Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val	
35 40 45	
gaa gca aga cag gtt tct aag aca gcc acc gat ggg tcc tac ctc ctc	371
Glu Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu	
50 55 60	
gta ttc aca tcc tat gta atc tcc tcc cca gtg tgg act gga cct ggt	419
Val Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly	
65 70 75	
gac ttg ctt cca gtg aat aga ata tagcaaaagt gattgatgtc acctccaaga	473
Asp Leu Leu Pro Val Asn Arg Ile	
80 85	
ttcagctata gaagactatg actatgactt tcctcttggc tagcattctc gctaaccctt	533
cctgcttgct tgtactgagc tgccctatga agaggcccat gtaggggtggc ctgggtgggg	593
gtgatctgtg gccaacagcc agcaaggaac taaatcctgt ttacaaccac atgagcttgg	653
aaggagatcc ttccccagta aagccaggag atgaatacaa aaaaaaaaaa aaa	706

<210> 195  
 <211> 670  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> 94..228

<400> 195

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acttttcagg ggacattcag aggcattcag cccttcctcc tcaccagctc ccagagttcc      60
catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc      114
                               Met Pro Arg Ser Ser Arg Ser
                               1           5
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr
      10           15           20
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga      210
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly
      25           30           35
cac ctc ccc aaa cat gaa tgacaacatc ctgttgccctg tccgcaacaa      258
His Leu Pro Lys His Glu
      40           45
tgaccaagcc ctaggcctga ctcagtgcac gctgggatgt gtgtcctggt tcacctgttt      318
tgctgtctcc ctgagaactc aggccagca gggtctgttt aacacgtgca gatgcaagct      378
gctgtgccag aagctcatgg agaagacagg cattctgtct ctctgtgctt tccgtgtgtc      438
ccagggccct gccagtcctc aggtggaagg tatccctggg ccctggcact gattatagga      498
cactgggcaa gacactgcac cgccacgtga ctcagtttcc ccatctgcct gatgggtgtt      558
gctgtgagaa ttatgaaatg aaatgatgac catgaaaata ttgtagaagc caagaaatgc      618
ttcagaagtt ataaagctct ccccaaaccg tgttatgaaa aaaaaaaaaa aa      670
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<210> 196

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..327

<400> 196

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aacctcaagg agccctgttg tgctaccgac tgcagagctc atggacatcc atcaggaagc      60
ctccaatacc caaaccaggg gtagttgcct aatccatcct catgtggata gctctttact      120
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata      171
                               Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile
                               1           5           10
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag      219
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln
      15           20           25
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc      267
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys
      30           35           40           45
agt tgc aga agt acc tgt gcc tct ttt tct tct tct tct tct tct      315
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser
      50           55           60
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt      367
Phe Leu Ile Ser
      65
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac      427
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tcttgttatt      487
tgcaatccaa aaaaaaaaaa aaa      510
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<210> 197

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..357

<400> 197

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atagaatata cacaaaagga a atg aga aag aaa tgt aaa tgc ttc act ata      51
                        Met Arg Lys Lys Cys Lys Cys Phe Thr Ile
                        1          5          10
aaa aaa aca aat aca tac gaa gaa agt aat gca gga aat gaa gga caa      99
Lys Lys Thr Asn Thr Tyr Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln
                        15          20          25
aaa gaa gct ata agc att tgt att tgc aga aga gat ggt tta ctt cct      147
Lys Glu Ala Ile Ser Ile Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro
                        30          35          40
ctg tgg gta acc agg tta tca gat ttg gtg ttt tcc aaa gaa aag gca      195
Leu Trp Val Thr Arg Leu Ser Asp Leu Val Phe Ser Lys Glu Lys Ala
                        45          50          55
cat ggc atg att cca ctt ctt ggc tcc cat agg gaa aag aag aca agt      243
His Gly Met Ile Pro Leu Leu Gly Ser His Arg Glu Lys Lys Thr Ser
                        60          65          70
aaa gag atg aag act tct tcc agg aac ctg agg tac ttc att gtc tgc      291
Lys Glu Met Lys Thr Ser Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys
                        75          80          85          90
aga gat gcc tca tcc tac acc cct cag tca ctc ata tct gga tac att      339
Arg Asp Ala Ser Ser Tyr Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile
                        95          100          105
gga cct tgt caa cat caa taatggacat acctctgata tttgaactct      387
Gly Pro Cys Gln His Gln
                        110
gaatctcact ctgtgaccac aactttgtat ctttctaagt ctttaatctt caacctcaca      447
gaactcttca taccctaaaa tatagtattt tcacctggaa aaaaaaaaaa aaa      500
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<210> 198

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..333

<400> 198

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aaa atg gtg ttt gga gcc atg gtc ctt ctt gtg gga ctt gaa gaa ctg      48
      Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu
      1          5          10          15
acc aat atc cgc aac gtg gag aga ctg aag aag gac ttg agg gcc agt      96
Thr Asn Ile Arg Asn Val Glu Arg Leu Lys Lys Asp Leu Arg Ala Ser
      20          25          30
tat tgc ctc atc gac agc ttc ctg ggg gac tgc gag ctc atc ggg gac      144
Tyr Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp
      35          40          45
ctg acc cag tgt gtg gac tgc gtg att cct cca gag ggg tcc ctc ttg      192
Leu Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu
      50          55          60
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct      240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro
```

65	70	75	
ggt gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt			288
Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu			
80	85	90	95
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga			333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly			
100	105	110	
tgaacggtag ctgctgcggt tacattatta gcttcagttt gcccgccag gctagatggt			393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaaagtga			453
ggaactcagg ctccagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct			513
ggctgtgggt ttctcccat tccctgcca tctgggaagt cgctgccacc ccctacgctt			573
gtctgctgac tcccagtcct cctaaccctc cagaatgtaa acagcagcag atgaacaaaa			633
ataaaaaatc aaaaggccga aaaaaaaaaa aaaa			667

<210> 199  
 <211> 514  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 1..363

<400> 199	
acg agt tct tcc ggg gcg gag gtc acc atg gca gct gcc ttg gct cgg	48
Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg	
1	5
ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc	96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe	
20	25
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt	144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser	
35	40
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg	192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val	
50	55
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg	240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly	
65	70
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc	288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu	
85	90
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg	336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly	
100	105
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca	383
Asp Lys Pro Gly Ala Asp Thr Gly Arg	
115	120
acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttcact taatcattca	443
aatcactatc tgaagggtca cggagcgcaa aataaagttt aaaaccctgc taccaaaaaa	503
aaaaaaaaa a	514

<210> 200  
 <211> 462  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS  
<222> 41..337

<400> 200

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cttcaccacc aaaactctcc actccaccag cacagccaaa atg ctc gca cgt gct      55
                                     Met Leu Ala Arg Ala
                                     1      5
act ttc cgc gcc gcc tcg gcc cca act ctc gtc gcc cgc cgc ggc ttc      103
Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
                                     10      15      20
cag tcg acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt      151
Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
                                     25      30      35
cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc      199
Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
                                     40      45      50
aag tac tgg ggc ttt atg ggc acc gga ttc gcc ctt ccc ttc ctc ctt      247
Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
                                     55      60      65
gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg      295
Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
                                     70      75      80      85
gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat      337
Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
                                     90      95
taggtggagg gcccgcatac ggctatacta gacatcacag catcaatttc attgtctgtc      397
ccccaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      457
aaaaa      462
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<210> 201  
<211> 551  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 1..549

<400> 201

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aga gag gga gcc cga gcc agg cca tct cca acc atg tcc gac gag gcc      48
Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1      5      10      15
tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc      96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20      25      30
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag      144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35      40      45
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc      192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50      55      60
cat cgc acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta      240
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65      70      75      80
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg      288
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
85      90      95
ttt tca tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta      336
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Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu	
100 105 110	
gat gat cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc	384
Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val	
115 120 125	
tgc agt gat gtc tct tct tct att agc act tac tgg gat tgg tca gat	432
Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp	
130 135 140	
agc gag ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt	480
Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser	
145 150 155 160	
gat gta ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg	528
Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu	
165 170 175	
ctt cct aaa aaa aaa aaa aa	551
Leu Pro Lys Lys Lys Lys Lys	
180	

<210> 202  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 34..315

<220>  
 <221> misc\_feature  
 <222> 483  
 <223> n=a, g, c or t

<400> 202	
agagaggggag cccgagccag gccatctcca acc atg tcc gac gag gcc tcg gcc	54
Met Ser Asp Glu Ala Ser Ala	
1 5	
atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc cca ctc	102
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu	
10 15 20	
ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc	150
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly	
25 30 35	
tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc	198
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg	
40 45 50 55	
acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct	246
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser	
60 65 70	
tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca	294
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser	
75 80 85	
tct gtc tgt tgg aga tca aga tgattgctat tccctgcttag atgatcagga	345
Ser Val Cys Trp Arg Ser Arg	
90	
cttcacttct ttgattttat ttcctgaggg gagggtctgc agtgatgtct cttcttctat	405
tagcacttac tgggattggc cagatagcga gtttgaatgg cagttaccag gcagtgacat	465
tgccagtggg agtgatgnta ctttctgatg tcataccagc tattccaagt tcaccttgcc	525
tgcttcctaa aaaaaaaaaa aaaaa	550

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..315

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 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu  
 1 5 10 15  
 ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt 96  
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly  
 20 25 30  
 ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144  
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly  
 35 40 45  
 ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192  
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly  
 50 55 60  
 acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 240  
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly  
 65 70 75 80  
 ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 288  
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe  
 85 90 95  
 atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335  
 Met Ala Ile Gly Met Gly Ile Arg Cys  
 100 105  
 atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagcaaaa 395  
 aaaaaaaaaa aaa 408

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 <212> DNA  
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 <222> 94..582

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 catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114  
 Met Pro Arg Ser Ser Arg Ser  
 1 5  
 cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162  
 Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg  
 10 15 20  
 ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag 210  
 Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu  
 25 30 35  
 gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac 258  
 Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn  
 40 45 50 55

aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc 306  
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser  
60 65 70  
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt 354  
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val  
75 80 85  
ctg ttt aac acg tgc aga tgc aag ctg ctg tgc cag aag ctc atg gag 402  
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu  
90 95 100  
aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct 450  
Lys Thr Gly Ile Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro  
105 110 115  
gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg 498  
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg  
120 125 130 135  
aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg 546  
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu  
140 145 150  
cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgacccat 592  
Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys  
155 160  
gaaaatattg tagaagccaa gaaatgcttc agaagttata aagctctccc caaacccgcaa 652  
aaaaaaaaaaa aaa 665  
  
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ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cctttcaaat ccgtctttgt 180  
gcccactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg 240  
gtctcttcgg aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc 300  
cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag 360  
ccccaccatg gtccttcggc ctcagcagtt ccaattctac cagccacagg ggatcacctc 420  
ctccccctca gccgtggtgg tggagatggg gtccaagcct gccctcacgg gggagcccgc 480  
cctcacgtgc atcagcaggg gcagtgaggg ggatccactc cgcggccagc tccctcatt 539  
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg 587  
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro  
1 5 10 15  
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga 635  
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg  
20 25 30  
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc 683  
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser  
35 40 45  
cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct 731  
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro  
50 55 60  
gaa cag cca gcc acc ctc aag gcg tcc cag cct gaa gca gcg tcc ttg 779  
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu  
65 70 75 80

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ggc cca gag atg acc gtc cta ttt gcc cac cga agt ggc tgc cac tcc      827
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
      85                      90                      95
gga cag cag aca gac ctc cgg aga aag tca gct ctt gcc aag gcc aca      875
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
      100                    105                    110
acc ctg gtg tcc act gcc tca ggc acg cag acc gtg ttt ccc agc aaa      923
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
      115                    120                    125
tgaacctacg ggtggctttt cctagacccc aaagaggtga attgcattta aatacagtct      983
gcctycactg aaaaaaaaaa aaaaaa                                     1008

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<210> 206  
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 <212> DNA  
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<220>  
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 <222> 77..364

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tttcaaccaa aacctc atg ctg acc aga gtt gag gaa cag aag aag atg gtg      112
      Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val
      1                      5                      10
aag gcc tgc agg tat agg tgt tca gca tgt cat ctg aaa tat tcc cca      160
Lys Ala Cys Arg Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro
      15                    20                    25
cag agg caa aaa gaa agg aaa tta tct ctg aaa agg ggg agg aca agt      208
Gln Arg Gln Lys Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser
      30                    35                    40
cag cag aat atg tca atg ttt tgg ttg aag aag ctg ctt gaa tct ggg      256
Gln Gln Asn Met Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly
      45                    50                    55                    60
ctt ttc tgt gcc atg tgt tct ccc agg gcc agc aca aag aag ggc ttt      304
Leu Phe Cys Ala Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe
      65                    70                    75
tgg tgc agg ccc aag acc acc ata atc atc att gat tat tcc tct cca      352
Trp Cys Arg Pro Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro
      80                    85                    90
cgc cag tgt ctc taaataaact ttctcttctt tctctgaaaa aaaaaaaaaa      404
Arg Gln Cys Leu
      95
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa a      455

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<210> 207  
 <211> 749  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 65..544

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<400> 207
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tacc atg ggg aaa atc gcg ctg caa ctc aaa gcc acg ctg gag aac atc      109

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Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile  
1 5 10 15  
acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg 157  
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met  
20 25 30  
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg 205  
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg  
35 40 45  
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg 253  
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met  
50 55 60  
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta 301  
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu  
65 70 75  
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag 349  
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys  
80 85 90 95  
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag 397  
Thr Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln  
100 105 110  
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca 445  
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser  
115 120 125  
gtg aca tta atc tgc agg aga agg act ggg act gac tat gat gaa aag 493  
Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys  
130 135 140  
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag 541  
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys  
145 150 155  
tgc tgatccctct tccttcccag ttgcccttaa gaactgagaa aggacaaagt 594  
Cys  
160  
actctaagca gcagagccca cagaggctcg ttcctttgac ccttgtctcc tgggtggctat 654  
acgaaacctt cacaatctgc atgctggact ttattacagc ttcccaagcc ccatcaataa 714  
agccctgttt cacgctacaa aaaaaaaaaa aaaaa 749

<210> 208  
<211> 594  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 117..467

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tgggcccccc actccccgcc gcaagtctg aggatggcca gcagagaaac aagaaa atg 119  
Met  
1  
gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg 167  
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val  
5 10 15  
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc 215  
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys  
20 25 30  
agc ctg cac agc cgg gcc ttt gga ctc ctg gat gct aga gtg acc tgg 263  
Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr Trp

35	40	45	
gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg			311
Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu			
50	55	60	65
ctt gca gca ttc cca gca gag gca tcg cct gtg gac acc gcg tct gtg			359
Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val			
70	75	80	
tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa			407
Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys			
85	90	95	
tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg			455
Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu			
100	105	110	
ggg ggt ata tcg taggtggcct taatacgtgt tatttgcctca tctgtatttc			507
Gly Gly Ile Ser			
115			
ttactctttg cacaattaaa ccatgttcct tttacttatg tacattttta ataaaagaaa			567
ggtgttaacg aaaaaaaaaa aaaaaaaa			594

<210> 209  
 <211> 2098  
 <212> DNA  
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<220>  
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 <222> 893..1897

<400> 209			
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ggcccgcggt tctcagggtc ttccataatcc cctgggcttt cgggcttgct gtgtgcctgg	180		
agtcaggccg ccgtgcggca ggctgttaac cttagcctcg ggagagtggg atggagccac	240		
cttctcatgg aacgatcctc gccttccctc atctccattg ttttatggct tcacacggac	300		
cgtggctttc tgcattggaag cttgggtggc aggggtgctgt cactttggga agcagccaga	360		
gaaccacagg atgcgtgaat cggctctcct gtcttcatgg gcatctccgg ccagggtggt	420		
gtcttgtgct gtgattagtg ggtcactggc aagtgtctga atgaagtgga gggtccgggtg	480		
gcaacagtga cggggaaggg ctatgggtcc gcctcaatgt catctgcccc atccctgggc	540		
ctccaggaat ccagggtctc agccctgctc ttagaaggaa gtcctgacgg ccacgctgga	600		
tctggaggac gtccggagct acagggcgga gatttcatct cgaaacctgg cggccagcag	660		
ggcagagccc taccacagag tgaagggtgga ctttgccctc tcgtgccacg aggacttgc	720		
ggcaccatc tctgagccca tcgagtggaa ataccacagc cctgaggagg agataagcct	780		
tggacctgcc tgctggctct gggatttttt aagacgaagt caacaggcag ggtttttgc	840		
gcccttgagt ggcgggggtgg acagcgcagc caccgcctgc ctcactact cc atg tgc	898		
	Met Cys		
	1		
tgc cag gtc tgc gag gcc gtg agg agt gga aat gag gaa gtg ctg gct	946		
Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val Leu Ala			
5	10	15	
gat gtc cgc acc atc gtg aac cag atc agc tac acc ccc cag gat ccc	994		
Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln Asp Pro			
20	25	30	
cga gac ctc tgt gga cgc ata ctg acc acc tgc tac atg gcc agc aag	1042		
Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala Ser Lys			
35	40	45	50
aac tcc tcc cag gag acg tgc acc cgg gcc aga gag ttg gcc cag cag	1090		
Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala Gln Gln			
55	60	65	

1138  
 1186  
 1234  
 1282  
 1330  
 1378  
 1426  
 1474  
 1522  
 1570  
 1618  
 1666  
 1714  
 1762  
 1810  
 1858  
 1907  
 1967  
 2027  
 2087  
 2098

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att gga agc cac cac atc agt ctc aac atc gat cca gcc gtg aag gcc 1138
Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val Lys Ala
      70      75      80
gtc atg ggc atc ttc agc ctg gtg acg ggg aag agc cct ctg ttt gca 1186
Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu Phe Ala
      85      90      95
gct cat gga gga agc agc agg gaa aac ctg gcg ctg caa aat gtg cag 1234
Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn Val Gln
      100      105      110
gct cga ata cgg atg gtc ctc gcc tat ctg ttt gct cag ttg agc ctc 1282
Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu Ser Leu
      115      120      125      130
tgg tct cgg ggt gtc cac ggt ggg ctc ctc gtg ctg gga tcc gcc aac 1330
Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser Ala Asn
      135      140      145
gtg gat gag agt ctc ctg ggc tac ctg acc aag tac gac tgc tcc agt 1378
Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser
      150      155      160
gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc 1426
Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala
      165      170      175
ttc gtc cag ttc tgc atc cag cgc ttc cag ctt cct gcc ctg cag agc 1474
Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser
      180      185      190
atc ctg ttg gcg ccg gcc acc gca gag ctg gag ccc ttg gct gat gga 1522
Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly
      195      200      205      210
cag gtg tcc cag acc gac gag gaa gat atg ggg atg aca tat gcg gag 1570
Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu
      215      220      225
ctc tcg gtc tat ggg aaa ctc agg aag gtg gcc aag atg ggg ccc tac 1618
Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly Pro Tyr
      230      235      240
agc atg ttc tgc aaa ctc ctc ggc atg tgg aga cac atc tgc acc ccg 1666
Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro
      245      250      255
aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg 1714
Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met
      260      265      270
aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac 1762
Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn
      275      280      285      290
tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac 1810
Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn
      295      300      305
aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag 1858
Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln
      310      315      320
ctc gag agg gca gag cca cag tcc ctg gac ggc gtg gac tgaggccggt 1907
Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp
      325      330      335
tccttcctgg aggcctcctg tcctcgggga cccagcacc tcctcatcag cattgctgga 1967
gccaagggtg ggagccctac actaggagcc caggatggga cggcgcatca gccgagaggg 2027
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 <211> 428

<212> DNA  
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<220>  
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<222> 85..342

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Met Cys Trp Val Ile Asn His Ala Ile  
1 5  
ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat 159  
Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His  
10 15 20 25  
tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag 207  
Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln  
30 35 40  
ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc 255  
Leu Cys Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe  
45 50 55  
agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc 303  
Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr  
60 65 70  
acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg 352  
Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg  
75 80 85  
aagcttgctg gcccacggag atgcagccgt ggagctgtga ggaaagacgg tctggcttca 412  
aaaaaaaa aaaaaa 428

<210> 211  
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atattggtgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa 175  
Met Lys Ile Ala Leu Cys Gln  
1 5  
aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act 223  
Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr  
10 15 20  
gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act 271  
Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr  
25 30 35  
gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc 319  
Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu  
40 45 50 55  
tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt 367  
Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys  
60 65 70  
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta 415

Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu  
                   75                                  80                                  85  
 cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg                  463  
 His Ser Leu Ser Ala Ala  
                   90  
 caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaaagca          523  
 ttaggcagat ggaatgtaca tgtgaggatg aggagacaga aaacaagtag ccctttccat          583  
 caagatagag ggttttctgg ggttgctggc tattgaatgt cactcctgat ttctctttcc          643  
 aaggcactgt accaccagcc tactgagatt gtgtgggagc tttcatgggg gttgtatttc          703  
 actgatgaaa ataaattttt tgcataatgt gaaaaaaaaa aaaaaaaaga aaaaaaaaaa          763  
 aaaaaa  769  
  
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     Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys  
         1                                  5                                  10                                  15  
 ttt gcc aag ctc acc aac acc tac tgt ctg gta gcg atc gga ggc tca          155  
 Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser  
                                   20                                  25                                  30  
 gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc          203  
 Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro  
                                   35                                  40                                  45  
 gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt          251  
 Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys  
                                   50                                  55                                  60  
 gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt          299  
 Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu  
                                   65                                  70                                  75  
 cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt          347  
 Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu  
                                   80                                  85                                  90                                  95  
 cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag          396  
 Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn  
                                   100                                  105  
 gatgagctgt cctctcttct tcaagtcccc cttgtggcgg ggactgtgaa ccgaggcagt          456  
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gccagaggag	taaaatttca	agagactgaa	accagatctg	agtttcgctg	ttccagtctg	360
gacctctttg	gtgctgtaaa	tcctggatat	actgtagatg	agtactgcgt	ttttctttta	420
tggactctct	tcagcttctg	gagacctcac	tatcctatt	atg tct ttg tgt gaa		474
				Met Ser Leu Cys Glu		
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gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc						522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly						
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tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc						570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly						
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agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt						618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser						
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acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca						666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser						
	55		60		65	
gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg						714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val						
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ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat						762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His						
	90		95		100	
cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat						810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His						
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ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat						858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp						
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gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta						906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val						
	135		140		145	
cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg						954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met						
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gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt						1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu						
	170		175		180	
agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca						1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro						
	185		190		195	
tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac						1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn						
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tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga						1146
Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly						
	215		220		225	

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Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala	
230 235 240 245	
cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa	1242
Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu	
250 255 260	
tta gag cag cag caa gtt tct agc agg gcc ttc aaa gta aaa aga att	1290
Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile	
265 270 275	
tgagccacgc atagtgtcac gcacctgtga tcccagctac ttaggaggtt gaggctggga	1350
ggatcacttg agcccaggag tctgaggctt tagtgatcta agatcatgcc actgcactcc	1410
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Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala	
15 20 25	
tac agc aaa gtg tat aca tta gac atc cct ctt ctc atg gtt cgc ctg	149
Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu	
30 35 40	
gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctc ttc cca	197
Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro	
45 50 55	
att cgt aca tca gtg atc aca ctg tta ttt ccc aaa cga ccc ttc agc	245
Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser	
60 65 70 75	
tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat	293
Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn	
80 85 90	
gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata	341
Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile	
95 100 105	
ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt	389
Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe	
110 115 120	
tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc	437
Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val	
125 130 135	
ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc	485
Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser	
140 145 150 155	
atg gca ctc att ata att gac tgg att tat gat cct cca aat tcc aag	533
Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys	
160 165 170	
cat cac taacacaagg aaaaatactt tctttttcta ttggaaatgg ttacaagtta	589

His His  
tactccaaaa gatatttgaa ttatcttgat tggaatgtta ttcataaggaa ataacaggaa 649  
gattccaaaag acgtttacca gtmatatcac caggcacctg cagaagagga aaatcactgt 709  
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Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe  
10 15 20  
aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct 150  
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala  
25 30 35  
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa 198  
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys  
40 45 50 55  
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga 246  
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly  
60 65 70  
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc 294  
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile  
75 80 85  
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg 342  
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu  
90 95 100  
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat 390  
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His  
105 110 115  
tat ctg atg tac ctg gtg atg gtg gca gcc ata gca tgg gag gaa act 438  
Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr  
120 125 130 135  
tat aga acc att ggc cta tat tgg gtt gga tct att att atg agt gtt 486  
Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val  
140 145 150  
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att 534  
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile  
155 160 165  
tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg 582  
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp  
170 175 180  
gct ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc 630  
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro  
185 190 195  
tca aag gtt att caa gaa gcc caa gcg aaa gac ctg aga aga cca 678  
Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro  
200 205 210 215

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Phe Asp Leu Met Leu Val Val Cys Leu Leu Leu Ala Thr Gly Phe Cys
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ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga      774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg
                235                240                245
tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat      822
Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr
                250                255                260
cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt      870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe
                265                270                275
gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct      918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro
280                285                290                295
gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct      966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser
                300                305                310
cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc     1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val
                315                320                325
cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga     1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly
                330                335                340
gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc     1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe
                345                350                355
ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taaaaatatt acttcatgtt     1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu
360                365                370
cctccttttct aaattactaa cttttgttat actgggtactg atattttgtc ccatttcact     1223
ctctttctcat acgtgagtac ttaagaatat gtacattctt gctctgcact gtatgtgtga     1283
gctatatggt attgtgtaaa ttttttttga agggaaatgg aaattcttga gaaacagttt     1343
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<222> 6..1184

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Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr
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ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att     146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile
                35                40                45
tac ctg gtc tcc ctg cca ttc gtg tgc ctc tgc ctc tat ttc tca ctg     194
Tyr Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu
50                55                60

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His Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro	
80 85 90 95	
agc atc atc tat gcc att gtg att gag atc atg aat cgt ctc tat cga	338
Ser Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg	
100 105 110	
tat gct gcc gag ttt tta act tca tgg gag aat cac aga ttg gaa tct	386
Tyr Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser	
115 120 125	
gcc tat cag aac cat cta att ctg aaa gtt tta gtg ttc aac ttc ctc	434
Ala Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu	
130 135 140	
aat tgc ttt gcc tca ctc ttc tat att gcc ttt gtc ttg aaa gat atg	482
Asn Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met	
145 150 155	
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Lys Leu Leu Arg Gln Ser Leu Ala Thr Leu Ile Thr Ser Gln Ile	
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Leu Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys	
180 185 190	
cat ggt gtg cgg gtg aag agg aag gtg cag gct tta aag gca gac att	626
His Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile	
195 200 205	
gat gct aca tta tat gaa caa gtc atc ctg gaa aaa gaa atg gga act	674
Asp Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr	
210 215 220	
tat ttg ggc acc ttt gat gat tac ttg gag tta ttc ctg cag ttt ggt	722
Tyr Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly	
225 230 235	
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Tyr Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala	
240 245 250 255	
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Val Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys	
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Arg Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val	
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Trp Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn	
290 295 300	
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Cys Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu	
305 310 315	
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Ser Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu	
320 325 330 335	
ctg gct tta aag ttt ata ctt gca ttt gcc ata cct gat aag cca cgg	1058
Leu Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg	
340 345 350	
cat atc cag atg aaa cta gcc aga ctg gaa ttt gag tct ttg gag gca	1106
His Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala	
355 360 365	
ctc aag cag cag caa atg aag ctc gtg acc gag aac ctg aag gag gaa	1154

Leu Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu  
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 Ala Val Glu Glu Leu Val Ser Gly Val Arg Gln Ala Ala Asp Phe Ala  
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 Glu Gln Phe Arg Ser Tyr Ser Glu Ser Glu Lys Gln Trp Lys Ala Arg  
 25 30 35 40  
 atg gaa ttc atc ctg cgc cac ctg ccc gac tac cgc gac ccg ccc gac 196  
 Met Glu Phe Ile Leu Arg His Leu Pro Asp Tyr Arg Asp Pro Pro Asp  
 45 50 55  
 ggc agt ggc cgc ctg gac cag ctg ctc tcc ctc tcc atg gtc tgg gcc 244  
 Gly Ser Gly Arg Leu Asp Gln Leu Leu Ser Leu Ser Met Val Trp Ala  
 60 65 70  
 aac cat ctc ttc cta ggc tgc agt tac aat aaa gac ctt tta gac aag 292  
 Asn His Leu Phe Leu Gly Cys Ser Tyr Asn Lys Asp Leu Leu Asp Lys  
 75 80 85  
 gtg atg gaa atg gcc gat ggg att gaa gtg gaa gac ctg cca caa ttt 340  
 Val Met Glu Met Ala Asp Gly Ile Glu Val Glu Asp Leu Pro Gln Phe  
 90 95 100  
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 Thr Thr Arg Ser Glu Leu Met Lys Lys His Gln Ser  
 105 110 115  
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gaatttttgt ttaaaatgcc tttttgggct gggccacagt ggccttatgc ccataataat 926
cccagcactt tgggaggccg aggtgagcag atcacctgag gttaggagtt tgagaccagc 986
ctggccaaca cgatgaaacc ccgctctctac taaaaatata aacaaaatta gctggggcatg 1046
gtggcggaaca tctgtaatcc cagctactca ggaggctgaa gcagaagaac tgcttgaacc 1106
tgggaggtgg aggttgcagt gagccaagat cgcaccattg cactccatcc tgggcgacaa 1166
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<210> 218
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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 78..566

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acaagacagc aagcagg atg gag cac tac cgg aaa gct ggc tct gta gag 110
Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu
1 5 10
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag 158
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu
15 20 25
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct 206
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala
30 35 40
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt 254
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly
45 50 55
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag 302
Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys
60 65 70 75
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag 350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln
80 85 90
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc 398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro
95 100 105
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg 446
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg
110 115 120
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc 494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro
125 130 135
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga 542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg
140 145 150 155
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgttctccg 596
Arg Arg Ala Arg Asp Thr Arg Ser
160
ggcctgaatg tctgggggtgc ttgtgccttt tctgagaagc gttgtgactg ctcaacatcc 656
ccatcaaggt ttgagtccac aaaagtggac ctccctatca tgcttcccct tccctctagc 716
atgtgggaag ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt 776
gctaaataag ggcttctctt gccttctacc tacagtgcac ttgaactgcc ttctgaaaga 836
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 <212> DNA  
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 agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag gtt 99  
 Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val  
                   15                  20                  25  
 ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta gaa 147  
 Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu  
                   30                  35                  40  
 gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat 195  
 Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn  
                   45                  50                  55                  60  
 ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg 243  
 Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala  
                   65                  70                  75  
 aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg 291  
 Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu  
                   80                  85                  90  
 ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca 339  
 Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala  
                   95                  100                  105  
 tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag ctt 387  
 Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu  
                   110                  115                  120  
 ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt 435  
 Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys  
                   125                  130                  135                  140  
 gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc 483  
 Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro  
                   145                  150                  155  
 agt tct ttg gct ttt act aaa aat gga cgc ctg gca acc aag tat cat 531  
 Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His  
                   160                  165                  170  
 acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg 579  
 Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr  
                   175                  180                  185  
 ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag 627  
 Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln  
                   190                  195                  200  
 att atg ttt gga ata tta aat ggt cta tac cat tat gca gta ttt gaa 675  
 Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu  
                   205                  210                  215                  220  
 gag aca ctt gag aaa act ata cat gaa gag taacacaaaaa aatgaatggt 725  
 Glu Thr Leu Glu Lys Thr Ile His Glu Glu  
                   225                  230  
 tgctaactta gcaaaatgaa gtttctataa agaggactca ggcatgtctg aaagagttaa 785  
 aagtaactgt gaacaaataa tttgttctgt gccttttggc tggtatatag caaataactca 845  
 aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa 905

aaaaa 910

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<213> Homo sapiens

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<222> 103..405

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Met Glu Arg Pro  
1  
gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa 162  
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu  
5 10 15 20  
agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta 210  
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe Phe Thr Ala Leu  
25 30 35  
atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata 258  
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile  
40 45 50  
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct 306  
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala  
55 60 65  
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg 354  
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val  
70 75 80  
tat gtg gcc tgg aat gaa ggc tca cga cag tgb cgt gaa ggc aaa cag 402  
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln  
85 90 95 100  
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat 455  
Asp  
aatgctggag ggggccatct gatttgaata aagttgaaag aacatgtaaa aaaaaaaaaa 515  
aaaa 519

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<212> DNA  
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<222> 72..350

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Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met  
1 5 10  
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc 158  
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr  
15 20 25  
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag 206  
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln

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Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu				
	50	55	60	
gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg				302
Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg				
	65	70	75	
aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc ggc ggg agg tca ccg				350
Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro				
	80	85	90	
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gcctttctcc ttcggtggcc cagcggagag tccggaccga gataccatgc caggactctc				470
cggggtctcg tgagctgccg tcgggtgagc acgtttcccc caaacctgg actgactgct				530
ttaagggtccg caaggcgggc cagggccgag acgcgagtcg gatgtggtga actgaaagaa				590
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Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys	
	10 15 20
ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg	151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu	
	25 30 35
gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg	199
Glu Ala Val Leu Lys Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro	
	40 45 50
gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag	247
Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln	
	55 60 65 70
acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt	295
Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys	
	75 80 85
gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct	343
Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala	
	90 95 100
aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga	391
Lys Lys Ala Phe Ala Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly	
	105 110 115
aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg	436
Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu	
	120 125 130
taggcctggt gaagaccacc tgggcccga gaggaactgg gggcaccctg agctccagta	496
ccaccactca caacaggcct cccagtggca gctcccagac ctggggcctg gccagggtc	556
taggggcccg cagtcttggg gtgggcoctg ccaattggga cgagtatccc tgatttgta	616
aaatgatgga aaaacgttca aaaaaaaaaa aaaaaa	652

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Ser	Ser	Tyr	Cys	Lys	Arg	Gly	Asn	Gly	Tyr	Arg	Ser	Arg	Val	Pro	Lys		
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Glu	Cys	Glu	Cys	Asn	Trp	Leu	His	Leu	Glu	Ser	Asp	Thr	Leu	Lys	Lys		
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Leu	Pro	Ile	Ile	Ser	Pro	Ser	Trp	Thr	Cys	Arg	Ile	Ile	Leu	Phe	Leu		
			60				65				70						
tat	ttt	tct	ggc	cag	ctt	ctc	caa	ctt	tcc	ctt	tct	tgt	ttg	caa	cta	471	
Tyr	Phe	Ser	Gly	Gln	Leu	Leu	Gln	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu		
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Ile	Lys	Leu															

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tgagctctga	ttcaagtgcc	tgcctctgcc	ccttggtggg	ctgaagcttc	atg gag											176	
					Met Glu												
					1												
gta	tcc	acc	aac	ccc	tcc	tcc	aac	atc	gat	cca	ggc	aac	tat	gtt	gaa	224	
Val	Ser	Thr	Asn	Pro	Ser	Ser	Asn	Ile	Asp	Pro	Gly	Asn	Tyr	Val	Glu		
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Met	Asn	Asp	Ser	Ile	Thr	His	Leu	Pro	Ser	Lys	Val	Val	Ile	Gln	Asp		
			20				25				30						
att	act	atg	gag	cta	cac	tgc	cct	ctg	tgc	aat	gat	tgg	ttc	cga	gac	320	
Ile	Thr	Met	Glu	Leu	His	Cys	Pro	Leu	Cys	Asn	Asp	Trp	Phe	Arg	Asp		
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cca	ctg	atg	cta	agc	tgt	ggc	cac	aac	ttc	tgt	gaa	gcc	tgt	atc	caa	368	
Pro	Leu	Met	Leu	Ser	Cys	Gly	His	Asn	Phe	Cys	Glu	Ala	Cys	Ile	Gln		
				55				60					65				
gac	ttt	tgg	agg	ctg	caa	gca	aag	gaa	aca	ttc	tgt	cct	gag	tgt	aag	416	
Asp	Phe	Trp	Arg	Leu	Gln	Ala	Lys	Glu	Thr	Phe	Cys	Pro	Glu	Cys	Lys		
			70				75					80					
atg	cta	tgt	cag	tat	aac	aac	tgt	aca	ttc	aac	cct	gta	ctg	gac	aag	464	
Met	Leu	Cys	Gln	Tyr	Asn	Asn	Cys	Thr	Phe	Asn	Pro	Val	Leu	Asp	Lys		
			85			90					95						
ttg	gta	gag	aag	att	aag	aag	tta	ccc	tta	ctc	aag	ggc	cat	cca	cag	512	
Leu	Val	Glu	Lys	Ile	Lys	Lys	Leu	Pro	Leu	Leu	Lys	Gly	His	Pro	Gln		
			100			105					110						
tgc	cca	gag	cat	gga	gag	aac	ctg	aaa	ctg	ttc	agt	aaa	cca	gat	ggg	560	
Cys	Pro	Glu	His	Gly	Glu	Asn	Leu	Lys	Leu	Phe	Ser	Lys	Pro	Asp	Gly		
					115		120			125			130				
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Lys	Leu	Ile	Cys	Phe	Gln	Cys	Lys	Asp	Ala	Arg	Leu	Ser	Val	Gly	Gln		
				135				140				145					
tct	aag	gag	ttc	ctg	caa	atc	tct	gat	gct	gtc	cat	ttc	ttc	atg	gag	656	
Ser	Lys	Glu	Phe	Leu	Gln	Ile	Ser	Asp	Ala	Val	His	Phe	Phe	Met	Glu		

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 Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys Glu Leu  
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 Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His Lys Glu  
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 Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu Lys Leu  
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 His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu Leu Arg  
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 Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu Ser Gln  
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 Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala Thr Arg  
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 Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly Pro Ile  
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 Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro Gly Leu  
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 Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu Val Leu  
 325  
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 Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys Ile Met  
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 Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val Ala Lys  
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 185  
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 His Val Ser Met Glu Phe Leu Lys Leu  
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 Lys Glu Lys Asp Ile Leu Thr Glu Leu Arg  
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 Glu Glu Met Glu Leu Asn Leu Ser Gln  
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 aag gat atg ttg gtg agc att cag  
 Lys Asp Met Leu Val Ser Ile Gln  
 250  
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 Ser Phe Asp Phe Leu Lys Asp Ile Thr  
 265  
 gga atg aag gtg ctg gca acc aga  
 Gln Gly Met Lys Val Leu Ala Thr Arg  
 280  
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 Leu Asn Leu Gly Gln Tyr Lys Gly Pro Ile  
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 Met Gln Asp Thr Leu Cys Pro Gly Leu  
 315  
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 Thr Ala His Pro Asn Leu Val Leu  
 330  
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 Thr His Gly Asp Ile Lys Lys Ile Met  
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 Asp Ser Ser Val Ala Val Leu Gly Ser  
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 Lys Trp Tyr Trp Glu Val Glu Val Ala Lys  
 380  
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 Glu Ser Ile Ile Arg Lys  
 395  
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 Gln Gly Phe Trp Leu Leu Arg Leu  
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 Ala Leu Asp Leu Pro Ser Phe Ser Leu  
 425  
 ggc ata tac ctg gat tat gaa  
 Val Gly Ile Tyr Leu Asp Tyr Glu  
 440  
 gct aaa acc atg act cac att tac  
 Asn Ala Lys Thr Met Thr His Ile Tyr  
 460  
 160  
 act ctg aag gag ctt  
 Thr Thr Leu Lys Glu Leu  
 175  
 gct gct cac aag gaa  
 Ala Ala His Lys Glu  
 190  
 gag ttt cta aag ctg  
 Glu Phe Leu Lys Leu  
 205  
 gag tta act gag ctc cgg  
 Thr Leu Thr Glu Leu Arg  
 220  
 gag ttg aat ctg agc cag  
 Leu Leu Asn Leu Ser Gln  
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 gtg agc att cag  
 Val Ser Ile Gln  
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 Lys Asp Ile Thr  
 270  
 gtg ctg gca acc aga  
 Val Leu Ala Thr Arg  
 285  
 ggt cct atc  
 Lys Gly Pro Ile  
 300  
 tac aaa ggt cct atc  
 Tyr Lys Gly Pro Ile  
 305  
 tgc cca ggc ctg  
 Cys Pro Gly Leu  
 320  
 aat ctg gtg ctc  
 Asn Leu Val Leu  
 335  
 aag aag ata atg  
 Lys Lys Ile Met  
 350  
 gta ctg ggc tca  
 Val Leu Gly Ser  
 370  
 gta gaa gta gca aag  
 Val Glu Val Ala Lys  
 385  
 atc att cgg aag  
 Ser Ile Ile Arg Lys  
 400  
 tta aga cta  
 Leu Leu Arg Leu  
 415  
 tct ttc agt ctg  
 Ser Phe Ser Leu  
 430  
 gat tat gaa  
 Leu Asp Tyr Glu  
 445  
 act cac att tac  
 Thr His Ile Tyr  
 465

gag ctt gcc atc caa cag ggt caa ctg gag aca act ctg aag gag ctt	704
Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys Glu Leu	
cag acc ctg agg aac atg cag aag gaa gct att gct gct cac aag gaa	752
Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His Lys Glu	
aac aag cta cat ctg cag caa cat gtg tcc atg gag ttt cta aag ctg	800
Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu Lys Leu	
cat cag ttc ctg cac agc aaa gaa aag gac att tta act gag ctc cgg	848
His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu Leu Arg	
gaa gag ggg aaa gcc ttg aat gag gag atg gag ttg aat ctg agc cag	896
Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu Ser Gln	
ctt cag gag caa tgt ctc tta gcc aag gat atg ttg gtg agc att cag	944
Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val Ser Ile Gln	
gca aag acg gaa caa cag aac tcc ttc gac ttt ctc aaa gac atc aca	992
Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys Asp Ile Thr	
act ctc tta cat agc ttg gag caa gga atg aag gtg ctg gca acc aga	1040
Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala Thr Arg	
gag ctt att tcc aga aag ctg aac ctg ggc cag tac aaa ggt cct atc	1088
Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly Pro Ile	
cag tac atg gta tgg agg gaa atg cag gac act ctc tgc cca ggc ctg	1136
Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro Gly Leu	
tct cca cta act ctg gac cct aaa aca gct cac cca aat ctg gtg ctc	1184
Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu Val Leu	
tcc aaa agc caa acc agc gtc tgg cat ggt gac att aag aag ata atg	1232
Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys Ile Met	
cct gat gat cct gag agg ttt gac tca agt gtg gct gta ctg ggc tca	1280
Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu Gly Ser	
aga ggc ttc acc tct gga aag tgg tac tgg gaa gta gaa gta gca aag	1328
Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val Ala Lys	
aag aca aaa tgg aca gtt gga gtt gtc aga gaa tcc atc att cgg aag	1376
Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile Arg Lys	
ggc agc tgt cct cta act cct gag caa gga ttc tgg ctt tta aga cta	1424
Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu Arg Leu	
agg aac caa act gat cta aag gct ctg gat ttg cct tct ttc agt ctg	1472
Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe Ser Leu	
aca ctg act aac aac ctc gac aag gtg ggc ata tac ctg gat tat gaa	1520
Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp Tyr Glu	
gga gga cag ttg tcc tac aat gct aaa acc atg act cac att tac	1568
Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His Ile Tyr	

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acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc 1616
Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
      470                      475                      480
tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat 1664
Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
      485                      490                      495
cca cag taatgagtca taatattata caaattcaga gtgttattaa agagggttttg 1720
Pro Gln
      500
aaataaaaaa aaaaaaaaaa 1739

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<210> 226
<211> 657
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 199..618

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<400> 226
aactggatag agtactgccc ccttcagccc atggagaaaag gcaaatgcct ccttcagagt 60
ctacctaatag ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct 120
aaaataagga atgaaatggtt ttcttgatat gattttttgt tttcatctga taataatttt 180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
                        Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
                        1                      5                      10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
      15                      20                      25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
      30                      35                      40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
      45                      50                      55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
      60                      65                      70                      75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
      80                      85                      90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
      95                      100                      105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
      110                      115                      120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
      125                      130                      135
tgc tagtactaat aaaaccaaca tgttaaaaaa aaaaaaaaaa 657
Cys
140

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<210> 227
<211> 888
<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> 182..481

<400> 227

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atattgcctc tcagtgttca agcttgagcc cacgcatcca actcctgaga tcttactggg      60
aagctgctga tcatcagttt caggaagtca gcatggatca gccttacgtt catggcctcc      120
aggccctatt ctctgcctc acagggaccg gccaggatct ctatccttac agcacgttgg      180
a atg tat atg ctc ctc tcc cca cat cgc ctt agg gag cag gca ggt gtc      229
  Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
    1         5         10        15
agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc      277
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
      20        25        30
cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc      325
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
      35        40        45
ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga      373
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
      50        55        60
cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca      421
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
      65        70        75        80
tct gca cct cct ctc aga gaa agc ctg atg cct act aaa gga ctt ggg      469
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
      85        90        95
tgg tgg acg cag tgaccctcag tctggagctt gttcactgaa cattggagac      521
Trp Trp Thr Gln
      100
tatcatttgc gcagatgggc ttgggcctct atgagcagca ggctgcaccc cacagtgacc      581
tcctcattct actctgaggg atcttcatga aagcagatgt ccattgaaaa gcacccaagt      641
gcagtctcag ctgatgaact tcagaggcga ttgagacaaa ggctctcggg cccctctgcc      701
cttggatggg gcctctggta tgcacttggc ctctgtgtct ttatttagac tggtcacttc      761
acaacccatc atgtcacccc acccctaacc gtgcccactc tgggtcctcc cctcaactgc      821
ctgacttccc actttgagct cagcaaaggc aatagatggt ttgtctgctt cgaaaaaaaa      881
aaaaaaaaa      888
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<210> 228

<211> 716

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..517

<400> 228

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acctgtcatt atgcttacta acgttcggga cgtctcccgg gctgcttggg cgaggagagg      60
caggggtgtg tgaccccggt gggtactgtg ctgcgctaga gcacctaggg cctgctgaag      120
ccctccctcg cccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc      175
      Met Ala Ser Tyr Ser
      1         5
ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc      223
Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly Pro Gly His Arg Ser
      10        15        20
tgc ctt ccc caa ttc gct ttc ttt ccg cag ccg ccg ctg ccc cga ccc      271
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Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro Pro Leu Pro Arg Pro  
 25 30 35  
 cgg atc tgc atg tgg gtg ctg gct gag ctg ctg gag cta ggg tgt cct 319  
 Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu Glu Leu Gly Cys Pro  
 40 45 50  
 gag cag agc ctg agg gac gcc atc acc ctg gac ctc ttc tgc cac gcg 367  
 Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp Leu Phe Cys His Ala  
 55 60 65  
 ctc att ttc tgc cgc cag cag ggc ttc tca ctg gag cag acg tca gcg 415  
 Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu Glu Gln Thr Ser Ala  
 70 75 80 85  
 gct tgt gcc ctg ctc cag gat ctt cac aag gct tgt att ggt gag agg 463  
 Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala Cys Ile Gly Glu Arg  
 90 95 100  
 ggg cag cta cca ggt ttg agc ccc agg gag aag agg aac cgg gcc tgg 511  
 Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys Arg Asn Arg Ala Trp  
 105 110 115  
 cac aag tgaccatggg aagcagaagc aggggatttc tgcctggaat atgtcattat 567  
 His Lys  
 tagtagcatc atcatacaca agccatcagc tttccaatcc actgcttcct tatctagaaa 627  
 ttaaggatac agcacacatt ttacaggact gttctgagaa ataatatatg caaatatatg 687  
 catagtgcac aataaaaaaaaa aaaaaaaaaa 716  
  
 <210> 229  
 <211> 654  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> 86..505  
  
 <400> 229  
 agttcgcggt gtcagcctcc gcctccgagc ctcagttgtc ttctctgtga ggtgggaatg 60  
 ccggtgaatc ctgccgctgg cgtgg atg aga agt gaa tgc gtg ctc gga gct 112  
 Met Arg Ser Glu Cys Val Leu Gly Ala  
 1 5  
 gcg agt gac agc ggg cag gag gcg ccc agg gac act tgg ttt ctc cag 160  
 Ala Ser Asp Ser Gly Gln Glu Ala Pro Arg Asp Thr Trp Phe Leu Gln  
 10 15 20 25  
 ggc tgg aag gct tct aga agg ttc ctc atc aag gga agt gtg gct ggg 208  
 Gly Trp Lys Ala Ser Arg Arg Phe Leu Ile Lys Gly Ser Val Ala Gly  
 30 35 40  
 ggc gcc gtc tac ctg gtg tac gac cag gag ctg ctg ggg ccc agc gac 256  
 Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly Pro Ser Asp  
 45 50 55  
 aag agc cag gca gcc cta cag aag gct ggg gag gtg gtc ccc ccc gcc 304  
 Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val Pro Pro Ala  
 60 65 70  
 atg tac cag ttc agc cag tac gtg tgt cag cag aca ggc ctg cag ata 352  
 Met Tyr Gln Phe Ser Gln Tyr Val Cys Gln Gln Thr Gly Leu Gln Ile  
 75 80 85  
 ccc cag ctc cca gcc cct cca aag att tac ttt ccc atc cgt gac tcc 400  
 Pro Gln Leu Pro Ala Pro Pro Lys Ile Tyr Phe Pro Ile Arg Asp Ser  
 90 95 100 105  
 tgg aat gca ggc atc atg acg gtg atg tca gct ctg tcg gtg gcc ccc 448  
 Trp Asn Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser Val Ala Pro  
 110 115 120

tcc aag gcc cgc gag tac tcc aag gag ggc tgg gag tat gtg aag gcg	496
Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala	
125 130 135	
cgc acc aag tagcgagtca gcaggggccc cctgccccgg ccagaacggg	545
Arg Thr Lys	
140	
cagggctgcc actgacctga agactccgga ctgggacccc actccgaggg cagctcccgg	605
ccttgccggc ccaataaagg acttcagaag tcaaaaaaaaa aaaaaaaaaa	654

<210> 230  
 <211> 635  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..382

<400> 230	
aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg	58
Met	
1	
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc	106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser	
5 10 15	
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca	154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr	
20 25 30	
ttt caa cag att cgg tgc tat tct gca cct gtt gct gct gag ccc ttt	202
Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro Phe	
35 40 45	
ctc agt ggg act agt tcg aac tat gtg gag gag atg tac tgt gct tgg	250
Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala Trp	
50 55 60 65	
ctg gaa aac ccc aaa agt gta cat aag aca ggg tcc cac tgt tgt cca	298
Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys Pro	
70 75 80	
ggc tgg agt gca gtg gcg gga tct cgg ctt gct gca acc tcc gac tcc	346
Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp Ser	
85 90 95	
tgg gtt caa gtg att ctt atg cct cag cct ccc gag taactgggac	392
Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu	
100 105	
tacaggtgca cgtcaccacg cctgactagt ttttgtatatt ttagtagaga tgggatttta	452
ctttgtttggc caggctgggc ttgaaccctt ggctcaagt gatccaccca ccttggcctc	512
ccaaagtgtc gggattacag gtatgatcaa ccacgcctgg ccatgtcatg ccttgtgaca	572
gaattccttt attctgtttt gagccaataa atatttatag gtttcgaaaa aaaaaaaaaa	632
aaa	635

<210> 231  
 <211> 634  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 56..355

<400> 231

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aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aacttcagga caaaa atg      58
                                         Met
                                         1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc      106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
                    5                10                15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca      154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
                20                25                30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc      202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Ser Pro Phe
                35                40                45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc      250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
                50                55                60                65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag      298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
                70                75                80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct      346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
                85                90                95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca      395
Gly Phe Lys
                100
ggtgcacgtc accacgcctg actagttttt gtatttttag tagagatggg attttacttt      455
ggtggccagg ctggtcttga acccctggcc tcaagtgatc caccacactt ggccctcccaa      515
agtgtctgga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat      575
tcctttattc tgttttgagc caataaatat ttataggttt cgaaaaaaaa aaaaaaaaaa      634
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<210> 232

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..498

<400> 232

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aatatagcca gccgcggctg cccttgcgct tcccgagctg gcgggggtccg tgggtgcggga      60
tcgagattgc gggct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc      111
                                         Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
                                         1                5                10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att      159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
                15                20                25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat      207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
                30                35                40
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg      255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
                45                50                55                60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc      303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile
                65                70                75
agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc      351
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu
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	80		85		90	
ggt ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac						399
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr						
	95		100		105	
ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg						447
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu						
	110		115		120	
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag						495
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys						
	125		130		135	
gtg tgagccctgt gcctgccggg acctccagcc tgcagaatgc gtccagaaat						548
Val						
aaattctgtg tctgtgtgaa aaaaaaaaaa aaaaaa						583

<210> 233  
 <211> 753  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 199..600

<400> 233	
atttttccga tgccaggcac cctcaaggca cagaggctgg ggctcatggt gggggcactt	60
ggcctctcca ggcctcgaag gcttctctgg gctgatgcga gctggggaac gggagggacg	120
gacgtgggag cgagaacgtc aacttgagg cagctgggtg cacgatgggg gacagagtga	180
aagagccttc gtgtcacc atg gcc aca cac ccc gat ggc ttc cgg ctt gag	231
Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu	
	1 5 10
gga ccc ctg gct gca gcc cac agc cct ggg cct tgc act gtg ctc tac	279
Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr	
	15 20 25
gaa ggc cct gtc cgt ggg ctc tgc ccy ttt gcc ccg cga aat tcc aac	327
Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn	
	30 35 40
acc atg gcg gcg gct gcc ctg gct gcc ccc agc ctg ggc ttc gat ggg	375
Thr Met Ala Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly	
	45 50 55
gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac atg cac gtg	423
Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp Met His Val	
	60 65 70 75
gtg gat gta gag ctg agc gga ccc cgg ggc ccc act ggc cga agc ttt	471
Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe	
	80 85 90
gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc gcg gtc acc	519
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr	
	95 100 105
ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg gcc tgc tgc	567
Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys	
	110 115 120
cag ctc ccc tcc agg ccg ggg atc cat ctc tgc tgagaagcct cctccctccc	620
Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys	
	125 130
gagacaagat catctgctg gcctctcacc accaccatcc caccctgcc ctgccccact	680
tccccagggt ctcccttctg actcagtaaa gatcaccgct gcctccccc gcaaataaaa	740
aaaaaaaaa aaa	753

<210> 234  
 <211> 762  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 211..612

<400> 234  
 atttccgatg ccaggcaccc tcaaggcaca gaggctgggg ctcatgttgg gggcacttgg 60  
 cctctccagg cctcgaaggc ttctcctggg ctgatgcgag ctggggaacg ggagggacgg 120  
 acgtgggagc gagaacgtca cactggaggc agctggtggc acgatggggg acagagtga 180  
 aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc 234  
 Met Ala Thr His Pro Asp Gly Phe  
 1 5  
 cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act 282  
 Arg Leu Glu Gly Pro Leu Ala Ala His Ser Pro Gly Pro Cys Thr  
 10 15 20  
 gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga 330  
 Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg  
 25 30 35 40  
 aat tcc aac acc atg tgc gcg gct gcc ctg gct gcc ccc agc ctg ggc 378  
 Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly  
 45 50 55  
 ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac 426  
 Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp  
 60 65 70  
 atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc 474  
 Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys  
 75 80 85  
 cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc 522  
 Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly  
 90 95 100  
 gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg 570  
 Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu  
 105 110 115 120  
 gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc 612  
 Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys  
 125 130  
 tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc accaccatcc 672  
 caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa gatcaccgct 732  
 gcctccccc gccaaaaaaa aaaaaaaaaa 762

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 ggt gga gag ccc cgg act gga gct cct gcg aac tcc cct tcc tgc cct 97

Gly Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro	
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cag gag atg cca ctg cag gac cca agg agc agg gag gag gcg gcc agg	145
Gln Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg	
35 40 45	
acc cag cag cta ttg ctg gcc act ctg cag gag gca gcg acc acg cag	193
Thr Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln	
50 55 60	
gag aac gtg gcc tgg agg aag aac tgg atg gtt ggc ggc gaa ggc ggc	241
Glu Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly	
65 70 75	
gcc agc ggg agg tca ccg tgagaccgga cttgcctccg tgggcgcggg	289
Ala Ser Gly Arg Ser Pro	
80 85	
accttggtt gggcgcagga atccgaggca gcctttctcc ttcgtgggcc cagcggagag	349
tccggaccga gataccatgc caggactctc cggggtcctg tgagctgccg tccgggtgagc	409
acgtttcccc caaaccttg actgactgct ttaagggtccg caaggcgggc cagggccgag	469
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aaaaaaaa	537
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Glu Ser Lys Ser Glu Glu Lys Met Trp Tyr Gly Val Phe Leu Trp Ala	
15 20 25	
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Leu Val Ser Ser Leu Phe Phe His Val Pro Ala Gly Leu Leu Ala Leu	
30 35 40	
ttc acc ctg aga cat cac aaa tat ggt agg ttc atg tct gta agc atc	196
Phe Thr Leu Arg His His Lys Tyr Gly Arg Phe Met Ser Val Ser Ile	
45 50 55	
ctg ttg atg ggc atc gtg gga cca att act gct gga atc ttg aca agt	244
Leu Leu Met Gly Ile Val Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser	
60 65 70	
gca gct att gct gga gtt tac cga gca gca ggg aag gaa atg ata cca	292
Ala Ala Ile Ala Gly Val Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro	
75 80 85 90	
ttt gaa gcc ctg aca ctg ggc act gga cag aca ttt tgc gtc ttg gtg	340
Phe Glu Ala Leu Thr Leu Gly Thr Gly Gln Thr Phe Cys Val Leu Val	
95 100 105	
gtc tcc ttt tta cgg att tta gct act cta tagcatacat ccttatgctg	390
Val Ser Phe Leu Arg Ile Leu Ala Thr Leu	
110 115	
agatgttgaa cttaaacttt atggaatcct ccaaaagaat acattatgga gtgtagtgtt	450
ttcttagttc ttcaaaggga agcaacttgg atgaacagga acatgaagga caacacatct	510
cagccttttc ttcatTTtga agctcctaga attgaagact tatgtggact cctattgttc	570
tcaacaaaa caagtctttt ggctttcttt tttgtagata tttaatttaa gcagttttca	630

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aactcttttc	tttgtctacat	cttagtgaca	ataaatgcc	aatagggttt	ggttgagtat	870
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<212> DNA
<213> Homo sapiens
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Gly Lys Ile Phe Val Ser Val Met Val Lys Leu Gln Lys Asn Lys Leu															
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acc tcc ttc ccc agg cag cca ttg tta aca ttt ttt gaa tat cta gaa	151														
Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe Phe Glu Tyr Leu Glu															
25 30 35															
aaa gtc ctt tgt tca gga tta ttt tcc cac tct gcc aag agt cac cat	199														
Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser Ala Lys Ser His His															
40 45 50															
gac ctg ctc aca cgc cac cct tat gaa act gcc gcg cca ctt ctc agc	247														
Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala Ala Pro Leu Leu Ser															
55 60 65															
tcc cat ttg att ctc aca gaa gct cta cga aat ggg ttg ggc aaa tgt	295														
Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn Gly Leu Gly Lys Cys															
70 75 80 85															
cat gat cct cat ttc aca ggg gaa gaa act gag gcc cag agg ggg aaa	343														
His Asp Pro His Phe Thr Gly Glu Glu Thr Glu Ala Gln Arg Gly Lys															
90 95 100															
ctg act acc taaaattgcc atgtaggccg gcgcggtggc tcacgcctgt															392
Leu Thr Thr															
aatcccagca ctgtgggagg ccaaggcggg tggatcgcga ggtcaggaga tcgagaccat	452														
cctggctggc acttgaagcc ccgtctctac tagggataca aataattggc cgggtgtggt	512														
ggcgggcgcg tgtgkwccca gctgttcggc aggctgagga gggcgaatgg tgtgagcctg	572														
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Leu Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln				
20	25	30		
aga gaa gcc caa cca gcc agc ccc cag gcc gcc ccg cca gga ccc acc				143
Arg Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr				
35	40	45		
aat gag gca cag atg gca gcc gct gcc gcc cta gcc cgg ctg gag cag				191
Asn Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln				
50	55	60		
aag cag tcc cgg gcc tgg ggc ccc aca tcg cag gac acc atc cga aac				239
Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn				
65	70	75		
cag gtg aga aag gaa ctt caa gcc gaa gcc acc gtc agc ggg agc ccc				287
Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro				
80	85	90	95	
gag gcc cca ggg acc aac gtg gta tct gag ccc aga gag gaa ggc tct				335
Glu Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser				
100	105	110		
gcc cac ctg gct gtg cct ggc gtg tac ttc acc tgt ccg ctc act ggg				383
Ala His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly				
115	120	125		
gcc acc ctg agg aag gac cag cgg gac gcc tgc atc aag gag gcc att				431
Ala Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile				
130	135	140		
ctc ttg cac ttc tcc acc gac cca gtg gcc gcc tcc atc atg aag atc				479
Leu Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile				
145	150	155		
tac acg ttc aac aaa gac cag gac cgg gtg aag ctg ggt gtg gac acc				527
Tyr Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr				
160	165	170	175	
att gcc aag tac ctg gac aac atc cac ctg cac ccc gag gag gag aag				575
Ile Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys				
180	185	190		
tac cgg aag atc aag ctg cag aac aag gtg ttt cag gag cgc att aac				623
Tyr Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn				
195	200	205		
tgc ctg gaa ggg acc cac gag ttt ttt gag gcc att ggg ttc cag aag				671
Cys Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln Lys				
210	215	220		
gtg ttg ctt ccc gcc cag gat cag gag gac ccc gag gag ttc tac gtg				719
Val Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val				
225	230	235		
ctg agc gag acc acc ttg gcc cag ccc cag agc ctg gag agg cac aag				767
Leu Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys				
240	245	250	255	
gaa cag ctg ctg gct gcg gag ccc gtg cgc gcc aag ctg gac agg cag				815
Glu Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg Gln				
260	265	270		
cgc cgc gtc ttc cag ccc tcg ccc ctg gcc tcg cag ttc gaa ctg cct				863
Arg Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu Pro				
275	280	285		
ggg gac ttc ttc aac ctc aca gca gag gag atc aag cgg gag cag agg				911
Gly Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln Arg				
290	295	300		
ctc agg tcc gag gcg gtg gag cgg ctg agc gtg ctg cgg acc aag gcc				959
Leu Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys Ala				

305	310	315	
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Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr			
320	325	330	335
ctg ctg cgc gtg cgc ctc ccc gat ggc tgc ctc ctg cag ggc act ttc			1055
Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe			
340	345	350	
tac gct cgg gag cgg ctg ggg gcg gtg tac ggg ttc gtc cgg gag gcc			1103
Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala			
355	360	365	
ctg cag agc gac tgg ctg cct ttt gag ctg ctg gcc tcg gga ggg cag			1151
Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln			
370	375	380	
aag ctg tcc gag gac gag aac ctg gcc ttg aac gag tgc ggg ctg gtg			1199
Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val			
385	390	395	
ccc tct gcc ctc ctg acc ttc tcg tgg gac atg gct gtg ctg gag gac			1247
Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp			
400	405	410	415
atc aag gcc gcg ggg gcc gag ccg gac tcc atc ctg aaa ccc gag ctc			1295
Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu			
420	425	430	
ctg tca gcc atc gag aag ctc ttg tgaaataaaaa gcagggttgg cctcagccct			1349
Leu Ser Ala Ile Glu Lys Leu Leu			
435			
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gcatgggtcc cgttcccgctg tgccgtgggt ggacgtggct gcacctggca ctagggtgc			1709
tctgtggatg tgggtgacaa cggcaggagg ggacgtggc cttcctgcac atagacctgc			1769
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taaaatgcca cggaagaacc tagggatgca ccaggaacca cgcgcctgaa tgccacaggt			180
ttgatttgat tcatgaccct catctggaca caagctctaa aatacttgag ccttggcaga			240
aatggctgat agagtccaca gaacacgtg tctcatctc agagaggaga actctgaacc			300
cagaggggaa ggatttacct gcagttgtat ggcaagccag aggtaggcgc tgcactggaa			360
cgcagcctaa ccagcctaaa gaaaccatgg gaggagaggc tcttaccctc tcctttgcag			420
atg tgg gcc cgg ctg cct cac act cca gag cag atg ggc cac agg ctt			468
Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu			
1	5	10	15
ata ggt ccc aag gaa gct tca ctt cat gtg gta ccc agc tgg cca gcc			516
Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala			
20	25	30	
agg aag atg gag ggg ctt ctg gct ggc ctc tct tcc tct cct aga aag			564

Arg	Lys	Met	Glu	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Ser	Ser	Pro	Arg	Lys		
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Ser	Cys	Trp	Pro	Phe	Trp	Val	His	Gly	Pro	Lys	Val	His	Glu	Gly	Gly		
		50					55					60					
tct	gcc	tgt	gag	aca	tca	agc	tcc	tgg	gtt	gaa	gga	ctt	gga	tta	aga	660	
Ser	Ala	Cys	Glu	Thr	Ser	Ser	Ser	Trp	Val	Glu	Gly	Leu	Gly	Leu	Arg		
		65				70				75				80			
aga	gtg	aca	tca	gtg	cac	agt	tta	tgc	caa	ggg	ctt	ggg	gcc	tca	gtc	708	
Arg	Val	Thr	Ser	Val	His	Ser	Leu	Cys	Gln	Gly	Leu	Gly	Ala	Ser	Val		
					85				90					95			
cag	ctt	ctt	cct	gga	cca	cca	cca	aca	aca	acc	agt	gat	aaa	aat	aat	756	
Gln	Leu	Leu	Pro	Gly	Pro	Pro	Pro	Thr	Thr	Thr	Ser	Asp	Lys	Asn	Asn		
			100					105				110					
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Tyr	Thr	Ser	Gly														

		115															
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Ile	Asp	Pro	Tyr	Gly	Phe	Glu	Arg	Pro	Glu	Asp	Phe	Asp	Asp	Ala	Ala		
			15				20					25					
tac	gag	aag	ttt	ttc	tcc	agc	tac	ctg	gtc	acg	ctc	acc	cgc	agg	gcg	206	
Tyr	Glu	Lys	Phe	Phe	Ser	Ser	Tyr	Leu	Val	Thr	Leu	Thr	Arg	Arg	Ala		
			30				35					40					
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Ile	Lys	Trp	Ser	Arg	Leu	Leu	Gln	Gly	Gly	Gly	Val	Pro	Arg	Ser	Arg		
		45				50					55						
aca	gtg	aag	cgc	tat	gtc	cgg	aaa	ggg	gtc	ccg	ctg	gag	cac	cgt	gcc	302	
Thr	Val	Lys	Arg	Tyr	Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala		
					60		65		70					75			
cgc	gtc	tgg	atg	gtg	ctg	agt	ggg	gcc	cag	gcg	cag	atg	gac	cag	aat	350	
Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn		
				80				85				90					
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg	398	
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu		
				95				100				105					
gag	gac	gcc	atc	agg	aca	gac	ctg	aac	cgg	acc	ttc	ccc	gac	aac	gtg	446	
Glu	Asp	Ala	Ile	Arg	Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val		
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Val Leu Leu Ala Tyr Gly His His Asn Gln Gly Val Gly Tyr Cys Gln
      140                      145                      150                      155
gga atg aat ttt ata gca gga tat ctg att ctt ata aca aat aat gaa      590
Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
      160                      165                      170
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      Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
      1                      5                      10
atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc      158
Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
      15                      20                      25
tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg      206
Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
      30                      35                      40
atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg      254
Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
      45                      50                      55
aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc      302
Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
      60                      65                      70                      75
cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat      350

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Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	
				80					85					90		
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg	398
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	
				95				100					105			
gag	gac	gcc	atc	agg	aca	gac	ctg	aac	cgg	acc	ttc	ccc	gac	aac	gtg	446
Glu	Asp	Ala	Ile	Arg	Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	
				110			115					120				
aag	ttc	cgg	aag	acc	acg	gac	ccc	tgc	tta	cag	agg	acc	ctg	tac	aat	494
Lys	Phe	Arg	Lys	Thr	Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	
				125			130				135					
gtg	ctg	ctg	gca	tat	ggg	cac	cat	aac	cag	gga	gtg	ggc	tac	tgc	cag	542
Val	Leu	Leu	Ala	Tyr	Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	
				140			145			150					155	
gga	atg	aat	ttt	ata	gca	gga	tat	ctg	att	ctt	ata	aca	aat	aat	gat	590
Gly	Met	Asn	Phe	Ile	Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp	
				160				165					170			
aag	aat	ctt	ttt	ggc	tgt	tagatgctct	tggttgaaga	atactaccag								638
Lys	Asn	Leu	Phe	Gly	Cys											
				175												
attactacag	cccgcccatg	ctgggcctga	agaccgacca	ggaggtcctc	ggggagctgg											698
tgcgggcgaa	gctgccggct	gtggggggccc	tgatggagcg	tctcgggtgtg	ctgtggacgc											758
tgctggtgtc	ccgctggttc	atctgcctgt	ttgtggacat	cttgcccgtg	gagacagtgc											818
ttcggatctg	ggactgtttg	tttaacgaag	gctcgaagat	tatcttccgg	ttggccctga											878
ccttaattaa	gcagcaccag	gagttgattt	tggaagccac	cagcgttcca	gacatttgcg											938
ataagtttaa	gcagataacc	aaagggagtt	tcgtgatgga	gtgtcacacg	tttatgcagg											998
tgtgtggggc	tgacagtggc	tcagtcacct	cccagggggc	cccgcctcac	ctgcagcccg											1058
ggggctgctc	tgaccaccgc	gaggatgcac	aggatgggca	ccagtgggca	tagggcacag											1118
gatgagcctc	cagctctgtc	ctgcactctgc	cccctgcgcc	tggcctccga	gggctttcct											1178
gtctatggcg	gcctgtgctt	cttggccctg	gcactgcgga	cgtgctcct	ggtcctaattg											1238
gctgtactca	tctgctgtgt	gtgggtgccag	aagtgtggct	tcccaggaggc	cggcctcccc											1298
actgggtcct	ggacctggcg	caggccgtat	agactcaggt	cctgatgagg	gcgttgtggg											1358
agctgtacct	gacaggcctt	ctgaggaagc	caagacgcc	ggagaggctc	aggcctggga											1418
gtcagtagtt	tcctaagagg	gagtgaggc	tcggggccac	tctgggtgca	gcatggcaaa											1478
cgtgggcggt	atttcagcag	ctgggccttc	atcaaagaga	agaccatgtt	ggccgggcgc											1538
ggtggctcac	gcctgcagtc	ccagcacttt	gggaggccaa	ggcgtgtgga	tcacctgagg											1598
tcaggagttc	aagaccagcc	tggccaacac	ggtgaaaccc	cgtctctact	aaaaaataca											1658
aaaattagcc	aggtgtggtg	gctcagcgtt	atgtagtccc	agttactcgg	gaggctgagg											1718
cacgagaatc	acttgaacct	gggaggcgga	ggttgacgtg	agccgagatc	gcgccactgc											1778
actccagcct	gggcaacaga	gtgagactct	gtctcaaaaa	aaaaaaaaaa	aa											1830

<210> 242  
 <211> 508  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27..-1

<400> 242  
 Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu  
 -25 -20 -15  
 Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro  
 -10 -5 1 5  
 Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp  
 10 15 20  
 Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser



<210> 243  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 243  
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe  
       -30                      -25                      -20  
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys  
       -15                      -10                      -5                      1  
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu  
                       5                      10                      15  
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg  
                       20                      25                      30  
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn  
       35                      40                      45  
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val  
       50                      55                      60                      65  
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His  
                       70                      75                      80  
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp  
                       85                      90                      95  
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg  
                       100                      105                      110  
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala  
                       115                      120                      125  
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys  
       130                      135                      140                      145  
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu  
                       150                      155                      160  
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu  
                       165                      170                      175  
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu  
                       180                      185                      190  
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg  
                       195                      200                      205  
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu  
       210                      215                      220                      225  
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser  
                       230                      235                      240  
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys  
                       245                      250                      255  
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe  
                       260                      265                      270  
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr  
       275                      280                      285  
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe  
       290                      295                      300

<210> 244  
 <211> 274  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17..-1

<400> 244

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Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
      -15              -10              -5
Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
  1          5          10          15
Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
      20          25          30
Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala
      35          40          45
Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala
      50          55          60
Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser
      65          70          75
Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val
  80          85          90          95
Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe
      100          105          110
Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr
      115          120          125
Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro
      130          135          140
Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val
      145          150          155
Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe
  160          165          170          175
Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met
      180          185          190
Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val
      195          200          205
Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly
      210          215          220
Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu
      225          230          235
Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys
  240          245          250          255
Ser Pro

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<210> 245  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35..-1

<400> 245

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Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro
-35          -30          -25          -20
Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
      -15          -10          -5
Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
  1          5          10
Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

```



Pro Ser Ala Ser Val Ile Arg Thr  
1 5

<210> 247  
<211> 348  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -29...-1

<400> 247  
Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met  
-25 -20 -15  
Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His  
-10 -5 1  
Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr  
5 10 15  
Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala  
20 25 30 35  
Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln  
40 45 50  
Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln  
55 60 65  
Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn  
70 75 80  
Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser  
85 90 95  
Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met  
100 105 110 115  
Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu  
120 125 130  
Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val  
135 140 145  
Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe  
150 155 160  
Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp  
165 170 175  
Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser  
180 185 190 195  
Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro  
200 205 210  
Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser  
215 220 225  
Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys  
230 235 240  
Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys  
245 250 255  
Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln  
260 265 270 275  
Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val  
280 285 290  
Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu  
295 300 305  
Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu  
310 315

<210> 248  
 <211> 397  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -36...-1

<400> 248  
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys Phe  
       -35                              -30                              -25  
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala  
       -20                              -15                              -10                              -5  
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val  
                               1                              5                              10  
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly  
       15                              20                              25  
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly  
       30                              35                              40  
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly  
       45                              50                              55                              60  
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile  
                               65                              70                              75  
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His  
                               80                              85                              90  
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly  
       95                              100                              105  
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu  
       110                              115                              120  
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu  
       125                              130                              135                              140  
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln  
                               145                              150                              155  
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala  
                               160                              165                              170  
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val  
       175                              180                              185  
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser Pro  
       190                              195                              200  
 Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp Glu  
       205                              210                              215                              220  
 Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser Val  
                               225                              230                              235  
 Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr Leu  
       240                              245                              250  
 Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr Glu  
       255                              260                              265  
 Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala Arg  
       270                              275                              280  
 Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile Lys  
       285                              290                              295                              300  
 Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys Ile  
                               305                              310                              315  
 Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg Glu  
       320                              325                              330  
 Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile Lys  
       335                              340                              345

Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser  
 350 355 360

<210> 249  
 <211> 403  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21..-1

<400> 249  
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val  
 -20 -15 -10  
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly  
 -5 1 5 10  
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu  
 15 20 25  
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser  
 30 35 40  
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser  
 45 50 55  
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg  
 60 65 70 75  
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu  
 80 85 90  
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val  
 95 100 105  
 Thr Ile Ser Cys Tyr Thr Arg Gly Arg Ile Ile Ser Thr Ser Ser  
 110 115 120  
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp  
 125 130 135  
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys  
 140 145 150 155  
 Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Val  
 160 165 170  
 Ser Glu Tyr Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys  
 175 180 185  
 Arg Ile Gln Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr  
 190 195 200  
 Gly Leu Arg Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile  
 205 210 215  
 Gly Val Ala Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser  
 220 225 230 235  
 Tyr Met Gln Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser  
 240 245 250  
 Leu Gln Val Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln  
 255 260 265  
 Arg Arg Ile Ser Ala His Gln Pro Gly Ala Gly Pro Glu Gly Gln Glu  
 270 275 280  
 Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu  
 285 290 295  
 Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu Glu Lys Pro Asp  
 300 305 310 315  
 Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp  
 320 325 330  
 Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala Asn Leu

335 340 345  
 Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu  
 350 355 360  
 Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys  
 365 370 375  
 Ser Ser Ser  
 380

<210> 250  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 250  
 Met Pro His Leu Met Glu Arg Met Val Gly Ser Gly Leu Leu Trp Leu  
 -25 -20 -15  
 Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser Ala Val Gln Arg Gly  
 -10 -5 1 5  
 Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly Leu Asp Leu Asp Cys  
 10 15 20  
 Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys Phe Asp Pro Cys Gln  
 25 30 35  
 Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr Arg Arg Gly Ala Gln  
 40 45 50  
 Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr Ala Gly Phe Leu Val  
 55 60 65 70  
 Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu Ala Trp Leu Phe  
 75 80 85

<210> 251  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 251  
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala  
 -15 -10 -5  
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr  
 1 5 10 15  
 Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys Ala Gly Gly Phe His Gly  
 20 25 30  
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Gly  
 35 40 45  
 Cys Leu Pro Asp Ser Ser Ser Ile  
 50 55

<210> 252  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15..-1

<400> 252  
 Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu  
 -15 -10 -5 1  
 Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala  
 5 10 15  
 Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala  
 20 25 30  
 Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser  
 35 40 45  
 Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu  
 50 55 60 65  
 Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu  
 70 75 80  
 Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly  
 85 90 95  
 Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu  
 100 105 110  
 Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala  
 115 120

<210> 253  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31..-1

<220>  
 <221> UNSURE  
 <222> 45  
 <223> Xaa = Glu,Gln

<220>  
 <221> UNSURE  
 <222> 44  
 <223> Xaa = Lys,Asn

<400> 253  
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe  
 -30 -25 -20  
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys  
 -15 -10 -5 1  
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu  
 5 10 15  
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg  
 20 25 30  
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn  
 35 40 45  
 Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser  
 50 55 60 65  
 Trp Thr Leu Ser Leu Leu Leu Thr Gly Phe Leu Ser

70

75

<210> 254  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24..-1

<400> 254  
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu  
                     -20                    -15                    -10  
 Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His  
                     -5                    1                    5  
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg  
   10                    15                    20  
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys  
 25                    30                    35                    40  
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile  
                     45                    50                    55  
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser  
                     60                    65                    70  
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro  
                     75                    80                    85  
 Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val  
   90                    95                    100  
 Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe  
 105                    110                    115                    120  
 Arg Arg Pro

<210> 255  
 <211> 381  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -33..-1

<400> 255  
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser  
                     -30                    -25                    -20  
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln  
                     -15                    -10                    -5  
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser  
   1                    5                    10                    15  
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu  
                     20                    25                    30  
 Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val  
                     35                    40                    45  
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu  
   50                    55                    60  
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met  
   65                    70                    75  
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys  
 80                    85                    90                    95

Ser Lys Asp Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr  
 100 105 110  
 Ala Gly Ala Arg Gln Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln  
 115 120 125  
 Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr  
 130 135 140  
 Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu  
 145 150 155  
 Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile  
 160 165 170 175  
 Gly Ser Gly Cys Asn Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly  
 180 185 190  
 Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly  
 195 200 205  
 Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala  
 210 215 220  
 Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp  
 225 230 235  
 Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr  
 240 245 250 255  
 Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser  
 260 265 270  
 Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His  
 275 280 285  
 Pro Val Ser Thr Ile Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val  
 290 295 300  
 Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu  
 305 310 315  
 Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser  
 320 325 330 335  
 Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu  
 340 345

<210> 256  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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<400> 256  
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser  
 -30 -25 -20  
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln  
 -15 -10 -5  
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser  
 1 5 10 15  
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu  
 20 25 30  
 Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val  
 35 40 45  
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu  
 50 55 60  
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met  
 65 70 75  
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val

Figure 1 consists of 12 histograms arranged in a single column. Each histogram represents the distribution of the number of non-zero elements in the vector  $x$  for a specific value of  $n$ . The x-axis for all histograms is labeled 'x' and ranges from 0 to 120. The y-axis is labeled 'count' and ranges from 0 to 100. The histograms are for  $n = 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120$ . As  $n$  increases, the distribution of  $x$  becomes more concentrated around zero, with the peak count increasing significantly.

Figure 1 consists of 12 bar charts arranged vertically, each representing a different birth cohort. The x-axis for all charts is 'Number of children' (0 to 10), and the y-axis is 'Percentage of women' (0 to 100). The cohorts are: 1910-1914, 1915-1919, 1920-1924, 1925-1929, 1930-1934, 1935-1939, 1940-1944, 1945-1949, 1950-1954, 1955-1959, 1960-1964, and 1965-1969. The distributions show a clear trend of decreasing fertility over time, with the peak number of children per woman moving from 4 in the 1910-1914 cohort to 2 in the 1965-1969 cohort.

<400> 258

Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro  
-20 -15 -10 -5  
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr  
1 5 10  
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys  
15 20 25  
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe  
30 35 40  
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro  
45 50 55 60  
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile  
65 70 75  
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr  
80 85 90  
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala  
95 100 105  
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn  
110 115 120  
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr  
125 130 135 140  
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile  
145 150 155  
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu  
160 165 170  
Asp Cys Asp Cys Glu Gln Cys Cys  
175 180

<210> 259

<211> 394

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39..-1

<400> 259

Met Ala Thr Ala Gln Leu Gln Arg Thr Pro Met Ser Ala Leu Val Phe  
-35 -30 -25  
Pro Asn Lys Ile Ser Thr Glu His Gln Ser Leu Val Leu Val Lys Arg  
-20 -15 -10  
Leu Leu Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe  
-5 1 5  
Pro Glu Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys  
10 15 20 25  
Ile Leu Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys  
30 35 40  
Trp Ile Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met  
45 50 55  
Val Val Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser  
60 65 70  
Glu Cys Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met  
75 80 85  
Asp Phe Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr  
90 95 100 105  
Asp Thr Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu  
110 115 120

Met	Gln	Asn	Leu	Gly	Pro	Leu	Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys
			125					130					135		
Leu	Phe	Tyr	Tyr	Asp	Glu	Val	Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly
		140					145					150			
Phe	Lys	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met
		155				160					165				
Tyr	Leu	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val
170					175					180					185
Lys	Val	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile
			190						195					200	
Leu	Ser	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp
		205					210					215			
Lys	Asp	Val	Glu	Asp	Glu	Gln	Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp
		220				225						230			
Ile	Glu	Thr	Lys	Met	Glu	Glu	Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu
		235				240					245				
Leu	Glu	Glu	Pro	Ser	Leu	Val	Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser
250					255					260					265
Lys	Glu	Ser	Pro	Asp	Leu	Ser	Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu
			270						275					280	
Val	Asn	Lys	Thr	Ser	Glu	Leu	Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser
		285					290						295		
Gly	Lys	Val	Phe	Gln	Asn	Lys	Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys
		300				305						310			
Ser	Ser	Lys	Glu	Asn	Arg	Lys	Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile
		315				320					325				
Val	Leu	His	His	Phe	Asp	Ser	Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg
330					335					340					345
Arg	Lys	Phe	Ser	Glu	Pro	Lys	Glu	His	Ile						
			350						355						

<210> 260  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> -17..-1

<400> 260  
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly  
           -15                          -10                          -5  
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met  
       1                          5                          10                          15  
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala  
                           20                          25                          30  
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr  
                           35                          40                          45  
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr  
                           50                          55                          60  
 Arg Val Val Ser Glu Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe  
       65                          70                          75  
 Thr Pro Arg Asn Ile Asp His Asp Pro Gln Glu Ile His Leu Glu Cys  
       80                          85                          90                          95  
 Ser Thr Ser Arg Lys Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn  
                           100                          105                          110  
 Glu Ile Lys Leu Asp Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr

[illegible]

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<220>
<221> SIGNAL
<222> -32..-1
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<210> 262
<211> 67
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -20..-1
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271

1 5 10  
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys  
 15 20 25  
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu  
 30 35 40  
 Glu Pro Ser  
 45

<210> 263  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 263  
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser  
 -25 -20 -15 -10  
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro  
 -5 1 5  
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg  
 10 15 20  
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser  
 25 30 35  
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro  
 40 45 50 55  
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser  
 60 65

<210> 264  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 264  
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys  
 -15 -10 -5  
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg  
 1 5 10  
 Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln  
 15 20 25  
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn  
 30 35 40 45  
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys  
 50 55 60  
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu  
 65 70 75  
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln  
 80 85 90  
 Leu Leu Arg Gln Glu His Glu Arg Leu Gln Lys Ile Ser Leu Glu  
 95 100 105  
 His Leu Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val

110 115 120 125  
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser  
 130 135 140  
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln  
 145 150 155

<210> 265  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 265  
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly  
 -15 -10 -5  
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met  
 1 5 10 15  
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala  
 20 25 30  
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr  
 35 40 45  
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr  
 50 55 60  
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln  
 65 70 75  
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe  
 80 85

<210> 266  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 266  
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly  
 -15 -10 -5  
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met  
 1 5 10  
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe  
 15 20 25 30  
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly  
 35 40 45  
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg  
 50 55 60  
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys  
 65 70 75  
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Ser Leu Ala  
 80 85 90  
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu  
 95 100 105

<210> 267  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 267  
 Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly Pro Pro Ile Ser Ser  
       -15                              -10                              -5  
 Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe Ser Arg Ala Thr Ser  
 1                              5                              10                              15  
 Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr Glu Ala Ser Ser Pro  
                               20                              25                              30  
 Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile Ile Val Arg Gln Gly  
                               35                              40                              45  
 Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser Leu Gly Asp Thr Gln  
                               50                              55                              60  
 His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile Tyr Arg Pro Trp Phe  
 65                              70                              75                              80  
 Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys Glu Ser Gln Leu Glu  
                               85                              90                              95  
 Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu Gly Lys Trp Asp Asn  
                               100                              105                              110  
 Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys Ser Ser Ser Ser  
                               115                              120                              125  
 Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys Lys Ser Arg His Gly  
                               130                              135                              140  
 Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met Ala Ser Arg Trp His  
 145                              150                              155                              160  
 Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala Cys Cys Arg Met Tyr  
                               165                              170                              175  
 Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys Arg Gly Phe Arg Glu  
                               180                              185                              190  
 Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu Lys Ala Leu Trp Ser  
                               195                              200                              205  
 Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu Ser Ser Gly Ser Cys  
                               210                              215                              220  
 Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg Gln Ile Gly Gly Glu  
 225                              230                              235                              240  
 Ala Tyr Leu Cys Leu  
                               245

<210> 268  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 268  
 Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu  
       -25                              -20                              -15                              -10  
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr

Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala Ser Arg Ser Ala Asp Gln  
 10 15 20  
 Ser Ser Gln Lys Val Lys Leu Arg Met Phe Thr Gly Arg Leu Pro Ile  
 25 30 35  
 Gly Pro Phe Ala Ser Val Gly Asn Ala Ala Glu Leu  
 40 45 50

<210> 269  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 269  
 Met Glu Thr Phe Pro Leu Leu Leu Ser Leu Gly Leu Val Leu Ala  
 -15 -10 -5  
 Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp  
 1 5 10 15  
 Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr  
 20 25 30  
 Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu  
 35 40 45  
 Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser  
 50 55 60  
 Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu  
 65 70 75 80  
 Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly  
 85 90 95  
 Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met  
 100 105 110  
 Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn Pro Gly  
 115 120 125  
 Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys Gln Phe  
 130 135 140  
 Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val Thr Ser  
 145 150 155 160  
 Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met Ser Trp  
 165 170 175  
 Leu Val Cys Gly Ser Lys Leu  
 180

<210> 270  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -36...-1

<400> 270  
 Met Ala Ser Val Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys  
 -35 -30 -25  
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser

-20					-15					-10					-5
Gly	Ile	Phe	Gly	Ala	Phe	Gln	Arg	Gly	Tyr	Tyr	Arg	Tyr	Tyr	Asn	Lys
				1				5					10		
Tyr	Ile	Asn	Val	Lys	Lys	Gly	Ser	Ile	Ser	Gly	Ile	Thr	Met	Val	Leu
		15					20					25			
Ala	Cys	Tyr	Val	Leu	Phe	Ser	Tyr	Ser	Phe	Ser	Tyr	Lys	His	Leu	Lys
	30					35					40				
His	Glu	Arg	Leu	Arg	Lys	Tyr	His								
45					50										

<210> 271  
 <211> 481  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25..-1

<400> 271

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Pro	Ser	Ile	Leu	Leu	Ala	Leu	Leu
-25					-20					-15					-10
Leu	Thr	Ser	Thr	Pro	Glu	Ala	Leu	Gly	Ala	Asn	Pro	Gly	Leu	Val	Ala
				-5				1				5			
Arg	Ile	Thr	Asp	Lys	Gly	Leu	Gln	Tyr	Ala	Ala	Gln	Glu	Gly	Leu	Leu
	10					15					20				
Ala	Leu	Gln	Ser	Glu	Leu	Leu	Arg	Ile	Thr	Leu	Pro	Asp	Phe	Thr	Gly
	25				30					35					
Asp	Leu	Arg	Ile	Pro	His	Val	Gly	Arg	Gly	Arg	Tyr	Glu	Phe	His	Ser
40					45				50					55	
Leu	Asn	Ile	His	Ser	Cys	Glu	Leu	Leu	His	Ser	Ala	Leu	Arg	Pro	Val
				60				65					70		
Pro	Gly	Gln	Gly	Leu	Ser	Leu	Ser	Ile	Ser	Asp	Ser	Ser	Ile	Arg	Val
		75				80						85			
Gln	Gly	Arg	Trp	Lys	Val	Arg	Lys	Ser	Phe	Phe	Lys	Leu	Gln	Gly	Ser
	90				95							100			
Phe	Asp	Val	Ser	Val	Lys	Gly	Ile	Ser	Ile	Ser	Val	Asn	Leu	Leu	Leu
	105				110						115				
Gly	Ser	Asp	Ser	Ser	Gly	Arg	Pro	Thr	Val	Thr	Ala	Ser	Ser	Cys	Ser
120					125					130				135	
Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp	Met	Ser	Gly	Asp	Leu	Gly	Trp
				140				145					150		
Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile	Glu	Ser	Lys	Phe	Gln	Lys	Val
		155				160						165			
Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile	Gln	Lys	Ser	Val	Ser	Ser	Asp
	170				175							180			
Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Thr	Val	Thr	Thr	Glu	Ile	Asp	Ser
	185				190						195				
Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	Glu	Ala	Pro	Arg	Ala	Thr	Ala
200					205					210				215	
Gln	Met	Leu	Glu	Val	Met	Phe	Lys	Gly	Glu	Ile	Phe	His	Arg	Asn	His
				220				225					230		
Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	Val	Met	Ser	Leu	Pro	Glu	Glu
		235				240						245			
His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	Ser	Asp	Tyr	Val	Phe	Asn	Thr
	250				255						260				
Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	Tyr	Leu	Asn	Phe	Ser	Ile	Thr
265					270						275				

Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	Ile	Arg	Leu	Thr	Thr	Lys	Ser
280					285					290					295
Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro	Asn	Met	Asn
			300						305					310	
Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu	Asn	Phe	Ser
			315					320					325		
Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	Met	Glu	Ile	Asp	Ala	Phe	Val
	330					335						340			
Leu	Leu	Pro	Ser	Ser	Ser	Lys	Glu	Pro	Val	Phe	Arg	Leu	Ser	Val	Ala
	345					350					355				
Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	Asn	Thr	Ser	Lys	Ile	Thr	Gly
360					365					370					375
Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	Glu	Leu	Lys	Glu	Ser	Lys	Val
				380					385					390	
Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	Ala	Leu	Leu	Asn	Tyr	Tyr	Ile
			395					400					405		
Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	Asp	Lys	Leu	Ala	Glu	Gly	Phe
	410						415					420			
Pro	Leu	Pro	Leu	Leu	Lys	Arg	Val	Gln	Leu	Tyr	Asp	Leu	Gly	Leu	Gln
	425					430					435				
Ile	His	Lys	Asp	Phe	Leu	Phe	Leu	Gly	Ala	Asn	Val	Gln	Tyr	Met	Arg
440					445					450					455
Val															

<210> 272  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -43..-1

Met	Ala	Lys	Tyr	Gln	Gly	Glu	Val	Gln	Ser	Leu	Lys	Leu	Asp	Asp	Asp
			-40					-35					-30		
Ser	Val	Ile	Glu	Gly	Val	Ser	Asp	Gln	Val	Leu	Val	Ala	Val	Val	Val
			-25				-20						-15		
Ser	Phe	Ala	Leu	Ile	Ala	Thr	Leu	Val	Tyr	Ala	Leu	Phe	Arg	Asn	Val
	-10					-5					1				5
His	Gln	Asn	Ile	His	Pro	Glu	Asn	Gln	Glu	Leu	Val	Arg	Val	Leu	Arg
				10					15					20	
Glu	Gln	Leu	Gln	Thr	Glu	Gln	Asp	Ala	Pro	Ala	Ala	Thr	Arg	Gln	Gln
			25					30					35		
Phe	Tyr	Thr	Asp	Met	Tyr	Cys	Pro	Ile	Cys	Leu	His	Gln	Ala	Ser	Phe
	40					45						50			
Pro	Val	Glu	Thr	Asn	Cys	Gly	His	Leu	Phe	Cys	Gly	Ala	Cys	Ile	Ile
	55					60					65				
Ala	Tyr	Trp	Arg	Tyr	Gly	Ser	Trp	Leu	Gly	Ala	Ile	Ser	Cys	Pro	Ile
70					75					80					85
Cys	Arg	Gln	Thr	Arg	His	Gly	His	Ile	Ala	Leu	Ser	Arg	Thr	Ala	
				90					95					100	

<210> 273  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 273

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Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
1          5          10          15
Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
          20          25          30
Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
          35          40          45
His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
          50          55          60
Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
65          70          75          80
Leu His
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<210> 274

<211> 373

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 274

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Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
          -25          -20          -15
Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile
          -10          -5          1          5
Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu
          10          15          20
Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile
          25          30          35
Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu
          40          45          50
Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly
          55          60          65
Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro
70          75          80          85
Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser
          90          95          100
Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly
          105          110          115
Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro
          120          125          130
Pro Gly Gly Gly Gly Glu Val Val Phe Ser Cys Pro Val Arg Lys Val
          135          140          145
Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg
150          155          160          165
Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile
          170          175          180
Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr
          185          190          195
Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly
          200          205          210
Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser
          215          220          225
Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro
230          235          240          245
Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Leu Glu Glu Ile Tyr
```

250 255 260  
 Arg Gly Gly Cys Val Asp Ser Thr Asn Gln Ser Leu Ala Leu Leu Leu  
 265 270 275  
 Met Thr Leu Gly Gln Gln Asp Val Ser Lys Val Leu Leu Gly Pro Leu  
 280 285 290  
 Ser Pro Tyr Thr Ile Glu Phe Leu Arg His Leu Lys Ser Phe Phe Gln  
 295 300 305  
 Ile Met Phe Lys Ile Glu Thr Lys Pro Cys Gly Glu Glu Leu Lys Gly  
 310 315 320 325  
 Gly Asp Lys Val Leu Met Thr Cys Val Gly Ile Gly Phe Ser Asn Leu  
 330 335 340  
 Ser Arg Thr Leu Lys  
 345

<210> 275  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25...-1

<400> 275  
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser  
 -25 -20 -15 -10  
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser  
 -5 1 5  
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly  
 10 15 20  
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly  
 25 30 35  
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His  
 40 45 50 55  
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly  
 60 65

<210> 276  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 276  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly  
 -20 -15 -10 -5  
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln  
 1 5 10  
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu  
 15 20 25  
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln  
 30 35 40  
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala  
 45 50 55 60  
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile

				65					70					75			
Lys	Cys	Leu	Gln	Thr	Thr	Glu	Glu	Pro	Pro	Ser	Arg	Thr	Ala	Gly	Ala		
			80					85					90				
Met	Met	Gln	Phe	Thr	Ala	Pro	Ile	Pro	Gly	Ala	Thr	Gly	Pro	Ile	Lys		
		95					100					105					
Leu	Ser	Gln	Lys	Thr	Ile	Val	Gln	Thr	Leu	Gly	Pro	Ile	Val	Gln	Tyr		
	110				115						120						
Pro	Gly	Ser	Asn	Gly	Arg	Ile	Asn	Ile	Ser	Gln	Leu	Thr	Ser	Glu	Asp		
125				130					135					140			
Leu	Thr	Gly	Ala	Lys	Gly	Arg	Val	Thr	Ser	Gly	Pro	Gln	Phe	Pro	Asn		
				145					150					155			
Ser	His	His	Val	Pro	Glu	Asn	Leu	His	Gly	Tyr	Met	Asn	Ser	Leu	Ser		
			160					165						170			
Leu	Phe	Ser	Pro	Ala													
			175														

<210> 277  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -29...-1

<400> 277

Met	Asp	Phe	Leu	Val	Leu	Phe	Leu	Phe	Tyr	Leu	Ala	Ser	Val	Leu	Met		
				-25					-20					-15			
Gly	Leu	Val	Leu	Ile	Cys	Val	Cys	Ser	Lys	Thr	His	Ser	Leu	Lys	Gly		
			-10					-5					1				
Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	Ser	Cys	Ile	Ile	Pro	Glu	Cys		
	5				10					15							
Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	His	Tyr	Leu	Phe	His	Thr	Arg		
20				25					30					35			
Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	Val	Leu	Gln	Gly	Met	Val	Tyr		
			40					45					50				
Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	Tyr	Cys	Gln	Glu	Leu	Glu	Leu		
			55					60					65				
Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Asn	Leu		
	70				75						80						
Phe	Phe	Phe	Thr	Leu	Thr	Cys	Gly	Thr	Asn	Pro	Gly	Ile	Ile	Thr	Lys		
	85				90				95								
Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	Tyr	Glu	Phe	Asp	Glu	Val	Met		
100				105					110					115			
Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	Cys	Asp	Leu	Arg	Lys	Pro	Ala		
			120						125					130			
Arg	Ser	Lys	His	Cys	Ser	Val	Cys	Asn	Trp	Cys	Val	His	Arg	Phe	Asp		
			135					140					145				
His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	Ile	Gly	Ala	Trp	Asn	Ile	Arg		
	150					155					160						
Tyr	Phe	Leu	Ile	Tyr	Val	Leu	Thr	Leu	Thr	Ala	Ser	Ala	Ala	Thr	Val		
	165				170					175							
Ala	Ile	Val	Ser	Thr	Thr	Phe	Leu	Val	His	Leu	Val	Val	Met	Ser	Asp		
180				185					190					195			
Leu	Tyr	Gln	Glu	Thr	Tyr	Ile	Asp	Asp	Leu	Gly	His	Leu	His	Val	Met		
			200					205					210				
Asp	Thr	Val	Phe	Leu	Ile	Gln	Tyr	Leu	Phe	Leu	Thr	Phe	Pro	Arg	Ile		
			215					220					225				

Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	Leu	Ser	Phe	Leu	Leu	Gly	Gly
		230					235					240			
Tyr	Leu	Leu	Phe	Val	Leu	Tyr	Leu	Ala	Ala	Thr	Asn	Gln	Thr	Thr	Asn
		245				250					255				
Glu	Trp	Tyr	Arg	Gly	Asp	Trp	Ala	Trp	Cys	Gln	Arg	Cys	Pro	Leu	Val
260					265					270					275
Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln	Val	His	Arg	Asn	Ile	His	Ser
				280					285					290	
His	Gly	Leu	Arg	Ser	Asn	Leu	Gln	Glu	Ile	Phe	Leu	Pro	Ala	Phe	Pro
			295					300					305		
Cys	His	Glu	Arg	Lys	Lys	Gln	Glu								
		310					315								

<210> 278  
 <211> 541  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28..-1

<400>	278														
Met	Gly	Ser	Gln	Glu	Val	Leu	Gly	His	Ala	Ala	Arg	Leu	Ser	Ser	Ser
			-25				-20					-15			
Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
		-10					-5					1			
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5				10					15						20
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
			25					30						35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45				50			
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
		55				60						65			
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
		70				75					80				
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90					95					100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105					110					115	
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
				185					190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200					205						210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
		215					220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val

245					250					255				260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe
				265					270					275
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln
			280					285					290	
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu
		295					300				305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser
	310					315					320			
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser
325				330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala
			345					350						355
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu
		360					365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe
	375					380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe
	390					395				400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu
405					410					415				420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala
			425					430						435
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly
		440					445					450		
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp
	455					460					465			
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala
	470				475					480				
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu
485				490				495						500
Thr	Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr		
			505					510						

<210> 279  
 <211> 267  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24..-1

<400> 279														
Met	Ala	Arg	Phe	Leu	Thr	Leu	Cys	Thr	Trp	Leu	Leu	Leu	Leu	Gly
				-20					-15					-10
Gly	Leu	Leu	Ala	Thr	Val	Arg	Ala	Glu	Cys	Ser	Gln	Asp	Cys	Ala
			-5					1			5			
Cys	Ser	Tyr	Arg	Leu	Val	Arg	Pro	Ala	Asp	Ile	Asn	Phe	Leu	Ala
	10				15					20				
Val	Met	Glu	Cys	Glu	Gly	Lys	Leu	Pro	Ser	Leu	Lys	Ile	Trp	Glu
25				30					35					40
Cys	Lys	Glu	Leu	Leu	Gln	Leu	Ser	Lys	Pro	Asp	Leu	Pro	Gln	Asp
			45					50					55	
Thr	Ser	Thr	Leu	Arg	Glu	Asn	Ser	Lys	Pro	Glu	Glu	Ser	His	Leu
		60					65					70		
Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Arg	Tyr	Gly	Gly	Phe	Met
	75					80					85			

Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu Glu Glu Ala Asn Gly  
 90 95 100  
 Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Lys Asp Ala  
 105 110 115 120  
 Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp Leu Leu Lys Glu Leu  
 125 130 135  
 Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His His Gln Asp Gly Ser  
 140 145 150  
 Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly Gly Phe Met Arg Gly  
 155 160 165  
 Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala Lys Glu Leu Gln Lys  
 170 175 180  
 Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg Pro Glu Trp Trp Met  
 185 190 195 200  
 Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys Arg Phe Ala Glu Ala  
 205 210 215  
 Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser Lys Glu Val Pro Glu  
 220 225 230  
 Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe  
 235 240

<210> 280  
 <211> 362  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -40...-1

<400> 280  
 Met Pro Phe Ala Tyr Phe Phe Thr Glu Ser Glu Gly Phe Ala Gly Ser  
 -40 -35 -30 -25  
 Arg Lys Gly Val Leu Gly Arg Val Tyr Glu Thr Val Val Met Leu Met  
 -20 -15 -10  
 Leu Leu Thr Leu Leu Val Leu Gly Met Val Trp Val Ala Ser Ala Ile  
 -5 1 5  
 Val Asp Lys Asn Lys Ala Asn Arg Glu Ser Leu Tyr Asp Phe Trp Glu  
 10 15 20  
 Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys Ile Ser Phe Leu Gly Val Leu  
 25 30 35 40  
 Leu Leu Leu Val Cys Thr Pro Leu Gly Leu Ala Arg Met Phe Ser Val  
 45 50 55  
 Thr Gly Lys Leu Leu Val Lys Pro Arg Leu Leu Glu Asp Leu Glu Glu  
 60 65 70  
 Gln Leu Tyr Cys Ser Ala Phe Glu Glu Ala Ala Leu Thr Arg Arg Ile  
 75 80 85  
 Cys Asn Pro Thr Ser Cys Trp Leu Pro Leu Asp Met Glu Leu Leu His  
 90 95 100  
 Arg Gln Val Leu Ala Leu Gln Thr Gln Arg Val Leu Leu Glu Lys Arg  
 105 110 115 120  
 Arg Lys Ala Ser Ala Trp Gln Arg Asn Leu Gly Tyr Pro Leu Ala Met  
 125 130 135  
 Leu Cys Leu Leu Val Leu Thr Gly Leu Ser Val Leu Ile Val Ala Ile  
 140 145 150  
 His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met  
 155 160 165  
 Gln Gly Thr Ser Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe

170		175		180
Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser				
185		190		200
Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg				
	205		210	215
Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu				
	220		225	230
Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu				
	235		240	245
Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly				
	250		255	260
Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr				
265		270		280
Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu				
	285		290	295
Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe				
	300		305	310
Pro Gln Ala Ser Arg Lys Thr Gln His Gln				
	315		320	

<210> 281  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 281
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
-20 -15 -10
Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln
-5 1 5 10
Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys
15 20 25
Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln
30 35 40
Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys
45 50 55
Ser
60

<210> 282  
 <211> 541  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 282
Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
-25 -20 -15
Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
-10 -5 1
Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn

5					10					15				20	
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
				25					30					35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45					50		
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
		55					60					65			
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70					75				80					
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90					95					100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105				110						115	
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
				185					190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200					205						210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
		215					220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235						240			
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250					255					260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
			265					270						275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
		280						285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
	295						300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
		360						365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
	375						380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
				425					430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
		440						445					450		
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp	Pro
	455						460				465				
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr

470		475		480
Leu Gly Thr Ala Phe	Leu Thr Glu Thr Lys	Leu Ile His Phe Leu Arg		
485	490	495		500
Thr Gln Leu Gly Val	Pro Arg Arg Thr Asp	Lys Met Thr		
505	510			

<210> 283  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 283

Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser	
-20 -15 -10	
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala	
-5 1 5 10	
Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg	
15 20 25	
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu	
30 35 40	
Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp	
45 50 55	
Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu	
60 65 70 75	
Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His	
80 85 90	
Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe	
95 100 105	
Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala	
110 115 120	
Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys	
125 130 135	
Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn	
140 145 150 155	
Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln	
160 165 170	
Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala	
175 180 185	
Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser	
190 195 200	
Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser	
205 210 215	
Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu	
220 225 230 235	
Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly	
240 245 250	
Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser	
255 260 265	
Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro	
270 275 280	
Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile	
285 290 295	
Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr	
300 305 310 315	



195	200	205
Val Pro Leu Gln Ser Lys	Asn Lys Leu Arg Lys	Arg Leu Ala Pro Leu
210	215	220
Val Tyr Val Gln Ser Tyr	Cys Asp Pro Pro Ser	Asp Arg Asp Ser Tyr
	230	235
Val Arg Glu Leu Met Thr	Tyr Ile Glu Val Asp	Ser Tyr Gly Glu Cys
	245	250
Leu Arg Asn Lys Asp Leu	Pro Gln Gln Leu Lys	Asn Pro Ala Ser Met
	260	265
Asp Ala Asp Gly Phe Tyr	Arg Ile Ile Ala Gln	Tyr Lys Phe Ile Leu
	275	280
Ala Phe Glu Asn Ala Val	Cys Asp Asp Tyr Ile	Thr Glu Lys Phe Trp
290	295	300
Arg Pro Leu Lys Leu Gly	Val Val Pro Val Tyr	Tyr Gly Ser Pro Ser
	310	315
Ile Thr Asp Trp Leu Pro	Ser Asn Lys Ser Ala	Ile Leu Val Ser Glu
	325	330
Phe Ser His Pro Arg Glu	Leu Ala Ser Tyr Ile	Arg Arg Leu Asp Ser
	340	345
Asp Asp Arg Leu Tyr Glu	Ala Tyr Val Glu Trp	Lys Leu Lys Gly Arg
	355	360
Ser Leu Thr Ser Asp Phe		
370	375	

<210> 285  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 285
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
40 45 50
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
55 60 65 70
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
75 80 85
Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
90 95 100
Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
105 110 115
Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
120 125 130
Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala
135 140 145 150
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
155 160 165

Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys  
170 175 180  
Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu  
185 190 195  
Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp  
200 205 210  
Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe  
215 220 225 230  
Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp  
235 240 245  
Val Leu Val Leu Leu Cys Gly Pro Pro Met Val Gln Leu Ala Cys  
250 255 260  
His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr  
265 270 275  
Tyr

<210> 286  
<211> 442  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21..-1

<220>  
<221> UNSURE  
<222> 132  
<223> Xaa = Pro,Arg

<400> 286  
Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser  
-20 -15 -10  
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala  
-5 1 5 10  
Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg  
15 20 25  
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu  
30 35 40  
Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp  
45 50 55  
Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu  
60 65 70 75  
Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His  
80 85 90  
Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe  
95 100 105  
Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala  
110 115 120  
Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys  
125 130 135  
Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn  
140 145 150 155  
Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln  
160 165 170  
Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala  
175 180 185  
Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser

	190		195		200										
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser
	205					210					215				
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu
220					225					230					235
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly
				240					245					250	
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser
		255					260					265			
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro
	270					275						280			
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile
	285					290				295					
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr
300				305					310						315
Arg	Glu	Glu	Leu	Gly	Gly	Ser	Pro	Ala	Gln	Val	Ser	Gly	Ala	Ser	Phe
				320					325					330	
Ser	Ser	Leu	Arg	Gln	Ser	Val	Ala	Gly	Thr	Tyr	Ser	Ile	Ser	Ser	Ser
		335					340					345			
Leu	Thr	Ala	Glu	Pro	Gly	Ser	Ala	Gly	Ala	Thr	Tyr	Thr	Cys	Gln	Val
	350					355						360			
Thr	His	Ile	Ser	Leu	Glu	Glu	Pro	Leu	Gly	Ala	Ser	Thr	Gln	Val	Val
	365				370				375						
Pro	Pro	Glu	Arg	Arg	Thr	Ala	Leu	Gly	Val	Ile	Phe	Ala	Ser	Ser	Leu
380				385					390						395
Phe	Leu	Leu	Ala	Leu	Met	Phe	Leu	Gly	Leu	Gln	Arg	Arg	Gln	Ala	Pro
				400				405						410	
Thr	Gly	Leu	Gly	Leu	Leu	Gln	Ala	Glu	Arg						
		415				420									

<210> 287  
 <211> 286  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -48..-1

<400> 287  
 Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser Ile Phe Asp Leu  
 -45 -40 -35  
 Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met Val Ala Gly Phe  
 -30 -25 -20  
 Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln Leu Ser Ser Ser  
 -15 -10 -5  
 Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu Lys Val Phe Trp  
 1 5 10 15  
 Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln Ser Thr Ala Ala  
 20 25 30  
 Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His Ala Asp Lys Ala  
 35 40 45  
 Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr Thr Ala Thr Gly  
 50 55 60  
 Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser Asn Leu Ile Phe  
 65 70 75 80  
 Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu Phe Ala Phe Leu  
 85 90 95

Gly	Phe	Leu	Gly	Cys	Leu	Val	Asn	Leu	Gln	Ala	Gly	His	Tyr	Leu	Ala
		100						105					110		
Met	Thr	Thr	Leu	Leu	Leu	Glu	Met	Ser	Thr	Pro	Phe	Thr	Cys	Val	Ser
		115					120					125			
Trp	Met	Leu	Leu	Lys	Ala	Gly	Trp	Ser	Glu	Ser	Leu	Phe	Trp	Lys	Leu
	130					135					140				
Asn	Gln	Trp	Leu	Met	Ile	His	Met	Phe	His	Cys	Arg	Met	Val	Leu	Thr
145				150						155					160
Tyr	His	Met	Trp	Trp	Val	Cys	Phe	Trp	His	Trp	Asp	Gly	Leu	Val	Ser
			165						170					175	
Ser	Leu	Tyr	Leu	Pro	His	Leu	Thr	Leu	Phe	Leu	Val	Gly	Leu	Ala	Leu
		180						185					190		
Leu	Thr	Leu	Ile	Ile	Asn	Pro	Tyr	Trp	Thr	His	Lys	Lys	Thr	Gln	Gln
		195					200					205			
Leu	Leu	Asn	Pro	Val	Asp	Trp	Asn	Phe	Ala	Gln	Pro	Glu	Ala	Lys	Ser
		210				215					220				
Arg	Pro	Glu	Gly	Asn	Gly	Gln	Leu	Leu	Arg	Lys	Lys	Arg	Pro		
225					230					235					

<210> 288  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
-20						-15					-10				
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1				5					10	
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu
			15					20					25		
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
	30					35						40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
	45					50					55				
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65					70					75
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
			80						85					90	
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
		95						100					105		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
	110						115						120		
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
	125					130					135				
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140					145					150					155
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr
			160						165					170	
Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln
		175						180					185		
Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg
	190						195					200			
Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala

205		210		215
Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln				
220		225		230
Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val				
	240		245	250
Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile				
	255		260	265
Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln				
	270		275	280
Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr				
	285		290	295
Glu Gly Gln Leu Ser Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser				
300		305		310
Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp				
	320		325	330
Glu Asp Ala Ala Leu Leu Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro				
	335		340	345
Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu Gly Ser Ser Glu Pro				
	350		355	360
Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys Ser Ser Ser				
365		370		375

<210> 289  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20...-1

<400> 289
Met Arg Gln Lys Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe
-20 -15 -10 -5
Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
1 5 10
Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
15 20 25
Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
30 35 40
Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
45 50 55 60
Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu
65 70 75
Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly
80 85 90
Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp
95 100 105
Glu Glu
110

<210> 290  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL

<222> -20..-1

<400> 290

Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly  
-20 -15 -10 -5  
Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met  
1 5 10  
Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu  
15 20 25  
Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile  
30 35 40  
Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp  
45 50 55 60  
Ser Glu Glu Asp Glu Glu  
65

<210> 291

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23..-1

<400> 291

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp  
-20 -15 -10  
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln  
-5 1 5  
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly  
10 15 20 25  
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys  
30 35 40  
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp  
45 50 55  
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe  
60 65 70  
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu  
75 80 85  
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp  
90 95 100 105  
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr  
110 115 120  
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys  
125 130 135  
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln  
140 145 150  
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg  
155 160 165  
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala  
170 175 180

<210> 292

<211> 111

<212> PRT

<213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 292  
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser  
                           -20                          -15                          -10  
 Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile  
                           -5                          1                          5  
 Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg  
       10                          15                          20  
 Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys  
 25                          30                          35                          40  
 Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys  
                           45                          50                          55  
 Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr  
                           60                          65                          70  
 Leu Met Val Ile Gln Asp Ile Thr Ala Met Val Arg Phe Asn Ile  
           75                          80                          85

<210> 293  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 293  
 Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu  
 -15                          -10                          -5                          1  
 Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys  
                           5                          10                          15  
 Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val  
       20                          25                          30  
 Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met  
       35                          40                          45  
 Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp  
 50                          55                          60                          65  
 Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe  
                           70                          75                          80  
 Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys  
                           85                          90                          95  
 Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr  
       100                          105                          110  
 Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp  
       115                          120

<210> 294  
 <211> 160  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

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<400> 294
Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu
  -25                      -20                      -15
Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile
  -10                      -5                      1                      5
Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg
                      10                      15                      20
Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu
                      25                      30                      35
Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile
                      40                      45                      50
Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile
                      55                      60                      65
Gly Leu Cys Leu Arg Val Lys Leu Gln Arg Cys Leu Pro Phe Lys His
70                      75                      80                      85
Lys Leu Glu Ile Tyr Ile Ser Glu Gly Thr His Ser Thr Glu Glu Asp
                      90                      95                      100
Ile Asn Lys Gln Ile Asn Asp Lys Glu Arg Val Ala Ala Ala Met Glu
                      105                      110                      115
Asn Pro Asn Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
                      120                      125                      130

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<210> 295
<211> 181
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -16...-1

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<400> 295
Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser
  -15                      -10                      -5
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn
1                      5                      10                      15
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro
20                      25                      30
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly
35                      40                      45
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys
50                      55                      60
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly
65                      70                      75                      80
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys
85                      90                      95
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr
100                      105                      110
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys
115                      120                      125
Gly Arg Glu Tyr Leu Pro Cys Ala Leu Phe Leu His Gln Gln Gly His
130                      135                      140
Arg Trp Ser Pro Lys Val Pro Asn Tyr Arg Ile Cys Ser Tyr Ser Gly
145                      150                      155                      160
Asn Tyr Ile Ser Ile
                      165

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<210> 296

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<211> 247  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18...-1

<400> 296  
 Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser  
                   -15                  -10                  -5  
 Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser Ile Ala  
           1                  5                  10  
 Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr  
 15                  20                  25                  30  
 Cys Cys Ala Pro Gln Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly  
                   35                  40                  45  
 Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro  
                   50                  55                  60  
 Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu  
           65                  70                  75  
 Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser  
           80                  85                  90  
 Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu  
 95                  100                  105                  110  
 Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val  
                   115                  120                  125  
 Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser  
                   130                  135                  140  
 Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His  
           145                  150                  155  
 Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp  
           160                  165                  170  
 Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu  
 175                  180                  185                  190  
 Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu  
                   195                  200                  205  
 Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly  
           210                  215                  220  
 Trp Thr Thr Trp Ala Arg Trp  
           225

<210> 297  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -41...-1

<400> 297  
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp  
           -40                  -35                  -30  
 Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser  
 -25                  -20                  -15                  -10  
 Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly Tyr  
                   -5                  1                  5

Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg Asn  
           10                          15                          20  
 Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe Leu  
           25                          30                          35  
 Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile Ser  
 40                          45                          50                          55  
 Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val Ser  
                           60                          65                          70  
 Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu Gly  
                           75                          80                          85  
 Cys Pro Gly Pro  
           90

<210> 298  
 <211> 251  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24...-1

<400> 298  
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val  
                           -20                          -15                          -10  
 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu  
                           -5                          1                          5  
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg  
           10                          15                          20  
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala  
 25                          30                          35                          40  
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala  
                           45                          50                          55  
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met  
                           60                          65                          70  
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn  
           75                          80                          85  
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His  
           90                          95                          100  
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala  
 105                          110                          115                          120  
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg  
                           125                          130                          135  
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg  
                           140                          145                          150  
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val  
           155                          160                          165  
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln  
           170                          175                          180  
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu  
 185                          190                          195                          200  
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly  
                           205                          210                          215  
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile  
           220                          225

<210> 299  
 <211> 137

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 299  
 Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly Arg  
           -20                          -15                          -10  
 Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly Pro Val  
       -5                          1                          5                          10  
 Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser Pro Glu Val  
                           15                          20                          25  
 Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val Pro Pro Gly Ser  
                           30                          35                          40  
 Glu Thr His Phe Arg Val Ala Val Val Ser Ser Arg Phe Glu Gly Leu  
                           45                          50                          55  
 Ser Pro Leu Gln Arg His Arg Leu Val His Ala Ala Leu Ala Glu Glu  
       60                          65                          70  
 Leu Gly Gly Pro Val His Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala  
 75                          80                          85                          90  
 Gln Trp Arg Glu Asn Ser Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly  
                           95                          100                          105  
 Gly Asn Lys Lys Thr Leu Gly Thr Pro  
                           110                          115

<210> 300  
 <211> 541  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28...-1

<400> 300  
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser  
           -25                          -20                          -15  
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn  
       -10                          -5                          1  
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn  
 5                          10                          15                          20  
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu  
                           25                          30                          35  
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser  
       40                          45                          50  
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp  
       55                          60                          65  
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp  
       70                          75                          80  
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu  
 85                          90                          95                          100  
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln  
                           105                          110                          115  
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val  
                           120                          125                          130  
 Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His

		135					140					145				
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	
	150					155					160					
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	
165					170					175					180	
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	
				185					190					195		
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	
			200					205					210			
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	
		215					220					225				
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	
	230					235					240					
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	
245					250					255					260	
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	
				265					270					275		
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	
			280					285					290			
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	
		295					300					305				
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	
	310					315					320					
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	
325					330					335					340	
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	
				345					350					355		
Asn	Gly	Val	Thr	Glu	Cys	Leu	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	
			360					365					370			
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	
		375					380					385				
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	
	390					395					400					
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	
405					410					415					420	
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	
				425					430					435		
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	
			440					445					450			
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro	
		455					460					465				
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	
	470					475					480					
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	
485					490											

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<210> 301
<211> 287
<212> PRT
<213> Homo sapiens
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<400> 301

Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln  
 -15 -10 -5  
 Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe  
 1 5 10 15  
 Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser  
 20 25 30  
 Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Tyr  
 35 40 45  
 Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Asp Met Met  
 50 55 60  
 Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn Lys Glu Asn Leu  
 65 70 75  
 Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro Ile Ser Pro Glu  
 80 85 90 95  
 Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr Arg Ser Ser Ala  
 100 105 110  
 Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly Ala Glu Glu Glu  
 115 120 125  
 Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe Pro Thr Cys Ser  
 130 135 140  
 Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg Gly Asp Leu Glu  
 145 150 155  
 Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu Gly Pro Ala Ala  
 160 165 170 175  
 Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu Arg Gly Pro Gln  
 180 185 190  
 Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr Met Met Val Asp  
 195 200 205  
 Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala Pro Lys Glu Ala  
 210 215 220  
 Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val Val Ser Thr Lys  
 225 230 235  
 Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala Glu Glu Met Lys  
 240 245 250 255  
 Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr Arg Phe His  
 260 265 270

<210> 302  
 <211> 165  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35..-1

<400> 302  
 Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro Pro His  
 -35 -30 -25 -20  
 Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro Pro Leu  
 -15 -10 -5  
 Ala Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr Gln Gly  
 1 5 10  
 Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg Gly Gly  
 15 20 25  
 Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala Cys Ala  
 30 35 40 45  
 Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val Trp Glu

				50					55					60			
Ser	Leu	Gln	Gln	Glu	Ala	Arg	Gln	Ala	Pro	Arg	Pro	Asn	Asn	Leu	His		
			65					70					75				
Thr	Leu	Cys	Gly	Ala	Pro	Val	His	Val	Arg	Glu	Arg	Gly	Thr	Gly	Ser		
		80					85					90					
Glu	Thr	Asn	Gln	Glu	Thr	Leu	Arg	Ala	Thr	Ala	Pro	Ala	Leu	Pro	Met		
	95					100					105						
Ala	Pro	Ala	Pro	Pro	Leu	Leu	Ala	Ala	Ala	Leu	Ala	Leu	Ala	Tyr	Leu		
110					115					120					125		
Leu	Arg	Pro	Leu	Ala													
				130													

<210> 303  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -25..-1

<400> 303																	
Met	Ala	Ser	Val	Val	Leu	Ala	Leu	Arg	Thr	Arg	Thr	Ala	Val	Thr	Ser		
-25					-20				-15						-10		
Leu	Leu	Ser	Pro	Thr	Pro	Ala	Thr	Ala	Leu	Ala	Val	Arg	Tyr	Ala	Ser		
				-5				1				5					
Lys	Lys	Ser	Gly	Gly	Ser	Ser	Lys	Asn	Leu	Gly	Gly	Lys	Ser	Ser	Gly		
	10					15						20					
Arg	Arg	Gln	Gly	Ile	Lys	Lys	Met	Glu	Gly	His	Tyr	Val	His	Ala	Gly		
	25				30						35						
Asn	Ile	Ile	Ala	Thr	Gln	Arg	His	Phe	Arg	Trp	His	Pro	Gly	Ala	His		
40				45					50						55		
Val	Gly	Val	Gly	Lys	Asn	Lys	Cys	Leu	Tyr	Ala	Leu	Glu	Glu	Gly	Ile		
				60				65						70			
Val	Arg	Tyr	Thr	Lys	Glu	Val	Tyr	Val	Pro	His	Pro	Arg	Asn	Thr	Glu		
			75				80						85				
Ala	Val	Asp	Leu	Ile	Thr	Arg	Leu	Pro	Lys	Gly	Ala	Val	Leu	Tyr	Lys		
	90					95						100					
Thr	Phe	Val	His	Val	Val	Pro	Ala	Lys	Pro	Glu	Gly	Thr	Phe	Lys	Leu		
	105				110						115						
Val	Ala	Met	Leu														
120																	

<210> 304  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34..-1

<400> 304																	
Met	Glu	Ser	Glu	Arg	Ser	Lys	Arg	Met	Gly	Asn	Ala	Cys	Ile	Pro	Leu		
				-30					-25					-20			
Lys	Arg	Ile	Ala	Tyr	Phe	Leu	Cys	Leu	Leu	Ser	Ala	Leu	Leu	Leu	Thr		
			-15					-10					-5				
Glu	Gly	Lys	Lys	Pro	Ala	Lys	Pro	Lys	Cys	Pro	Ala	Val	Cys	Thr	Cys		



<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -30..-1

<400> 306  
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val  
 -30 -25 -20 -15  
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp  
 -10 -5 1  
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu  
 5 10 15  
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu  
 20 25 30  
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu  
 35 40 45 50  
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser  
 55 60 65  
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val  
 70 75 80  
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly  
 85 90 95  
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala  
 100 105 110  
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile  
 115 120 125 130  
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu  
 135 140 145  
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu  
 150 155 160  
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu  
 165 170 175  
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu  
 180 185 190  
 Ile Asn Lys Ser Gly Glu Lys Ala Met  
 195 200

<210> 307  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20..-1

<400> 307  
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe  
 -20 -15 -10 -5  
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser  
 1 5 10  
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly  
 15 20 25  
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala  
 30 35 40  
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala

45                      50                      55                      60  
 Ile Leu Asn Gly Gly  
                                 65

<210> 308  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -43...-1

<400> 308  
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys  
                                 -40                      -35                      -30  
 Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly  
                                 -25                      -20                      -15  
 Ser Leu Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr  
                                 -10                      -5                      1                      5  
 Ser Ser Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys  
                                 10                      15                      20  
 Leu Gly Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys  
                                 25                      30                      35  
 Glu Asp Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro  
                                 40                      45                      50  
 Pro Leu Lys Ser Glu Lys His Glu Glu  
                                 55                      60

<210> 309  
 <211> 291  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 309  
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu  
                                 -30                      -25                      -20  
 Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr  
                                 -15                      -10                      -5  
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys  
                                 1                      5                      10  
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr  
                                 15                      20                      25                      30  
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Val Phe Thr  
                                 35                      40                      45  
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu  
                                 50                      55                      60  
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile  
                                 65                      70                      75  
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys  
                                 80                      85                      90  
 Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu  
                                 95                      100                      105                      110  
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys

				115				120					125				
Gly	Leu	Asp	Ser	Leu	Thr	Asn	Val	Asp	Leu	Arg	Gly	Asn	Ser	Phe	Asn		
			130					135					140				
Cys	Asp	Cys	Lys	Leu	Lys	Trp	Leu	Val	Glu	Trp	Leu	Gly	His	Thr	Asn		
		145					150					155					
Ala	Thr	Val	Glu	Asp	Ile	Tyr	Cys	Glu	Gly	Pro	Pro	Glu	Tyr	Lys	Lys		
	160					165				170							
Arg	Lys	Ile	Asn	Ser	Leu	Ser	Ser	Lys	Asp	Phe	Asp	Cys	Ile	Ile	Thr		
175				180					185						190		
Glu	Phe	Ala	Lys	Ser	Gln	Asp	Leu	Pro	Tyr	Gln	Ser	Leu	Ser	Ile	Asp		
			195						200					205			
Thr	Phe	Ser	Tyr	Leu	Asn	Asp	Glu	Tyr	Val	Val	Ile	Ala	Gln	Pro	Phe		
		210					215						220				
Thr	Gly	Lys	Cys	Ile	Phe	Leu	Glu	Trp	Asp	His	Val	Glu	Lys	Thr	Phe		
	225					230				235							
Arg	Asn	Tyr	Asp	Asn	Ile	Thr	Val	Leu	Arg	Glu	Ile	His	Arg	Phe	Thr		
	240					245					250						
Asn	Met	Ser															
255																	

<210> 310  
 <211> 426  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -28..-1

<400>	310																
Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly		
			-25					-20					-15				
Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln	Val	Gly	Gly	His	Ser	Cys	Val		
		-10					-5					1					
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Leu	Cys	Lys	Pro	Leu	Val	Pro	Arg	Glu		
5				10					15					20			
His	Gln	Phe	Tyr	Glu	Thr	Leu	Pro	Ala	Glu	Met	Arg	Lys	Phe	Thr	Pro		
			25					30						35			
Gln	Tyr	Lys	Gly	Val	Val	Ser	Val	Arg	Phe	Glu	Glu	Asp	Glu	Asp	Arg		
		40					45					50					
Asn	Leu	Cys	Leu	Ile	Ala	Tyr	Pro	Leu	Lys	Gly	Asp	His	Gly	Ile	Val		
	55					60					65						
Asp	Ile	Val	Asp	Asn	Ser	Asp	Cys	Glu	Pro	Lys	Ser	Lys	Leu	Leu	Arg		
	70				75				80								
Trp	Thr	Thr	Asn	Lys	Lys	His	His	Val	Leu	Glu	Thr	Glu	Lys	Thr	Pro		
85				90					95					100			
Lys	Asp	Trp	Val	Arg	Gln	His	Arg	Lys	Glu	Glu	Lys	Met	Lys	Ser	His		
			105					110						115			
Lys	Leu	Glu	Glu	Glu	Phe	Glu	Trp	Leu	Lys	Lys	Ser	Glu	Val	Leu	Tyr		
		120					125					130					
Tyr	Thr	Val	Glu	Lys	Lys	Gly	Asn	Ile	Ser	Ser	Gln	Leu	Lys	His	Tyr		
	135					140					145						
Asn	Pro	Trp	Ser	Met	Lys	Cys	His	Gln	Gln	Gln	Leu	Gln	Arg	Met	Lys		
	150				155				160								
Glu	Asn	Ala	Lys	His	Arg	Asn	Gln	Tyr	Lys	Phe	Ile	Leu	Leu	Glu	Asn		
165				170					175					180			
Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly		
			185				190							195			

Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln
			200					205						210	
Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val
		215					220					225			
Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met
		230				235					240				
Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Met	Gln	Gly	Phe	Lys	Glu	Ala
245					250					255					260
Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu
			265						270					275	
Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg
		280						285					290		
Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp
		295					300					305			
Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu
		310				315					320				
Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala
325					330					335					340
Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe
			345						350					355	
Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu
			360					365					370		
Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile
		375				380						385			
Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu						
		390				395									

<210> 311  
 <211> 466  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -16...-1

<400> 311  
 Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser  
 -15 -10 -5  
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn  
 1 5 10 15  
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala  
 20 25 30  
 Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys  
 35 40 45  
 Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu  
 50 55 60  
 Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly  
 65 70 75 80  
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His  
 85 90 95  
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro  
 100 105 110  
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys  
 115 120 125  
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser  
 130 135 140  
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly



Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu  
 50 55 60  
 Gly Lys Gly Phe Arg Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly  
 65 70 75 80  
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His  
 85 90 95  
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro  
 100 105 110  
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys  
 115 120 125  
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser  
 130 135 140  
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly  
 145 150 155 160  
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro  
 165 170 175  
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu  
 180 185 190  
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro  
 195 200 205  
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys  
 210 215 220  
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala  
 225 230 235 240  
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala  
 245 250 255  
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala  
 260 265 270  
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu  
 275 280 285  
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu  
 290 295 300  
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Ala  
 305 310 315 320  
 Ser Ser Ser Glu Pro Cys Ala Thr Arg Ser Leu Ser Leu Pro Cys Ser  
 325 330 335  
 Gly Ser Ser Thr Pro Arg Ala Pro Ser Ala Arg Arg Arg Met Lys Thr  
 340 345 350  
 Trp Cys Glu Met Arg Cys Ser Arg Thr Arg Ala Pro Ser Gly  
 355 360 365

<210> 313

<211> 258

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -36...-1

<400> 313

Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe  
 -35 -30 -25  
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala  
 -20 -15 -10 -5  
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val  
 1 5 10  
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly





<400> 316  
Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu  
-15 -10 -5  
Cys Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp  
1 5 10 15  
Glu Leu Arg Thr Asp Phe Lys Ser Pro Ile Asp Gln Cys Asn Pro Val  
20 25 30  
His Ala Arg Glu Arg Leu Arg Asn Ile Glu Arg Ile Cys Phe Leu Leu  
35 40 45  
Arg Lys Leu Val Leu Pro Glu Tyr Ser Ile His Ser Leu Phe Cys Ile  
50 55 60  
Met Phe Leu Cys Ala Gln Glu Trp Leu Thr Leu Gly Leu Asn Val Pro  
65 70 75  
Leu Leu Phe Tyr His Phe Trp Arg Tyr Phe His Cys Pro Ala Asp Ser  
80 85 90 95  
Ser Glu Leu Ala Tyr Asp Pro Pro Val Val Met Asn Pro Asp Thr Leu  
100 105 110  
Ser Tyr Cys Gln Lys Glu Ala Trp Cys Lys Leu Ala Phe Tyr Leu Leu  
115 120 125  
Ser Phe Phe Tyr Tyr Leu Tyr Cys Met Ile Tyr Thr Leu Val Ser Ser  
130 135 140

<210> 317  
<211> 426  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -28...-1

<400> 317  
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly  
-25 -20 -15  
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val  
-10 -5 1  
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu  
5 10 15 20  
His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys Phe Thr Pro  
25 30 35  
Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg  
40 45 50  
Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val  
55 60 65  
Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg  
70 75 80  
Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro  
85 90 95 100  
Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His  
105 110 115  
Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr  
120 125 130  
Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr  
135 140 145  
Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys  
150 155 160  
Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn  
165 170 175 180

Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly  
 185 190 195  
 Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln  
 200 205 210  
 Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val  
 215 220 225  
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met  
 230 235 240  
 Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala  
 245 250 255 260  
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu  
 265 270 275  
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg  
 280 285 290  
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp  
 295 300 305  
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu  
 310 315 320  
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala  
 325 330 335 340  
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe  
 345 350 355  
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu  
 360 365 370  
 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile  
 375 380 385  
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu  
 390 395

<210> 318  
 <211> 301  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20..-1

<400> 318  
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val  
 -20 -15 -10 -5  
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln  
 1 5 10  
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg  
 15 20 25  
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile  
 30 35 40  
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu  
 45 50 55 60  
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe  
 65 70 75  
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met  
 80 85 90  
 Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln  
 95 100 105  
 Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val  
 110 115 120  
 Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly

125					130					135					140
Lys	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Trp	Glu	Phe	Ala	Ala	Arg	Gly	Gly
				145					150					155	
Leu	Lys	Gly	Gln	Val	Tyr	Pro	Trp	Gly	Asn	Trp	Phe	Gln	Pro	Asn	Arg
			160					165					170		
Thr	Asn	Leu	Trp	Gln	Gly	Lys	Phe	Pro	Lys	Gly	Asp	Lys	Ala	Glu	Asp
		175					180					185			
Gly	Phe	His	Gly	Val	Ser	Pro	Val	Asn	Ala	Phe	Pro	Ala	Gln	Asn	Asn
	190					195					200				
Tyr	Gly	Leu	Tyr	Asp	Leu	Leu	Gly	Asn	Val	Trp	Glu	Trp	Thr	Ala	Ser
205					210					215				220	
Pro	Tyr	Gln	Ala	Ala	Glu	Gln	Asp	Met	Arg	Val	Leu	Arg	Gly	Ala	Ser
			225					230					235		
Trp	Ile	Asp	Thr	Ala	Asp	Gly	Ser	Ala	Asn	His	Arg	Ala	Arg	Val	Thr
		240				245						250			
Thr	Arg	Met	Gly	Asn	Thr	Pro	Asp	Ser	Ala	Ser	Asp	Asn	Leu	Gly	Phe
	255					260					265				
Arg	Cys	Ala	Ala	Asp	Ala	Gly	Arg	Pro	Pro	Gly	Glu	Leu			
270					275						280				

<210> 319  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -17...-1

<400> 319															
Met	Gly	Ser	Gly	Trp	Leu	Thr	Ala	Val	Ala	Ser	Leu	Leu	Pro	Ser	Pro
		-15					-10				-5				
Gly	Asn	Ser	Glu	Leu	Pro	Val	Gln	Ala	Leu	Gly	Arg	Arg	Gly	Gly	Arg
1				5					10					15	
Asp	Trp	Ala	Arg	Asn	Glu	Ala	Gly	Arg	Asp	Leu	Glu	Lys	Pro	Pro	Arg
			20					25					30		
Leu	His	Cys	Ser	Gly	Arg	Gly	Arg	Leu	Glu	Glu	Pro	Val	Pro	Pro	Asn
		35				40						45			
His	Leu	Pro	Val	Gly	Leu	Ser	Val	Arg	Gly	Ser	Gln	Val	Leu	Ser	Ser
	50					55					60				
Ala	Gly	Pro	Arg	Arg	Cys	Arg	Leu	Thr	Gly	Thr	Arg	Asn	Pro	Val	Arg
	65				70				75						
Gly	Pro	Arg	Arg	Val	Glu	Gln	Ile	Ala	Arg	Gly	Gly	Pro	Glu	Ala	Arg
80					85				90					95	
Arg	Gln	Ala	Gly	Asp	Ser	Cys									
			100												

<210> 320  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -39...-1

<400> 320  
 Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His

				-35					-30					-25			
Ala	Phe	Ala	Asp	Gly	Ala	Trp	Asp	Leu	Ser	Phe	Leu	Cys	Ala	Leu	Cys		
			-20					-15					-10				
Ser	Phe	Cys	Pro	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Pro	Tyr	Arg	Tyr	Leu		
		-5					1				5						
Glu	Phe	Trp	Arg	Leu	Tyr	Leu	Ser	Pro	Ser	Ser	Met	Glu	Asn	Gly	Val		
10					15					20					25		
Gln	Lys	Phe	His	Glu	Thr	Phe	Phe	Ile	Val	Phe	Leu	Leu	Leu	Phe	Asp		
				30					35					40			
Ile	Glu	Arg	Lys	Gly	Lys	Ser	Ser	Val	Cys	Pro	Phe	Cys	Tyr	Arg			
			45					50					55				

<210> 321  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -39..-1

<400> 321																	
Met	Met	Thr	Ile	Thr	Phe	Leu	Pro	Tyr	Thr	Phe	Ser	Leu	Met	Val	Thr		
				-35				-30						-25			
Phe	Pro	Asp	Val	Pro	Leu	Gly	Ile	Phe	Leu	Phe	Cys	Val	Cys	Val	Ile		
			-20					-15					-10				
Ala	Ile	Gly	Val	Val	Gln	Ala	Leu	Ile	Val	Gly	Tyr	Ala	Phe	His	Phe		
		-5					1				5						
Pro	His	Leu	Leu	Ser	Pro	Gln	Ile	Gln	Arg	Ser	Ala	His	Arg	Ala	Leu		
10					15				20						25		
Tyr	Arg	Arg	His	Val	Leu	Gly	Ile	Val	Leu	Gln	Gly	Pro	Ala	Leu	Cys		
				30				35						40			
Phe	Ala	Ala	Ala	Ile	Phe	Ser	Leu	Phe	Phe	Val	Pro	Leu	Ser	Tyr	Leu		
			45					50					55				
Leu	Met	Val	Thr	Val	Ile	Leu	Leu	Pro	Tyr	Val	Ser	Lys	Val	Thr	Gly		
		60					65					70					
Trp	Cys	Arg	Asp	Arg	Leu	Leu	Gly	His	Arg	Glu	Pro	Ser	Ala	His	Pro		
	75				80						85						
Val	Glu	Val	Phe	Ser	Phe	Asp	Leu	His	Glu	Pro	Leu	Ser	Lys	Glu	Arg		
90					95				100					105			
Val	Glu	Ala	Phe	Ser	Asp	Gly	Val	Tyr	Ala	Ile	Val	Ala	Thr	Leu	Leu		
				110				115						120			
Ile	Leu	Asp	Ile	Cys	Pro	Ser	Cys	Ser	Leu	Trp	Leu	Ala	Val	Ala	Ser		
			125				130					135					
Phe	Gln	Arg	Leu	Leu	Leu	Arg	Gly	Leu	Ile	Cys	Leu	Phe	Val	Cys			
		140					145					150					

<210> 322  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -41..-1

<400> 322  
 Met Pro Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp

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      -40      -35      -30
Asp Ser Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu
-25      -20      -15      -10
Ala Gln Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val
      -5      1      5
Met Ser Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser
      10      15      20
Gly Thr Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser
      25      30      35
Ser Arg Leu Thr Phe Gln Arg Arg Phe
40      45

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<210> 323
<211> 70
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -38..-1

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<400> 323
Met Ser Ser Pro Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu
      -35      -30      -25
Thr Thr Ala Ile Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe
      -20      -15      -10
Phe Thr Pro Leu Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys
      -5      1      5      10
Val Thr Lys Asp Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys
      15      20      25
Glu Ala Thr Trp Leu Pro
      30

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<210> 324
<211> 168
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> -25..-1

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<400> 324
Met Arg Gly Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu
-25      -20      -15      -10
Leu Val Val Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp
      -5      1      5
Glu Arg Leu Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu
      10      15      20
Val Leu Ala Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met
      25      30      35
Leu Ala Ala Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe
40      45      50      55
Leu Ile Ala Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala
      60      65      70
Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
      75      80      85
Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala

```

```

          90                      95                      100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
    105                      110                      115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
120                      125                      130                      135
Cys Trp Ile Pro Ser Pro Pro Ala
                      140

```

<210> 325  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

```

<400> 325
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15                      -10                      -5                      1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
    5                      10                      15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
    20                      25                      30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
    35                      40                      45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
    50                      55                      60                      65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
    70                      75                      80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
    85                      90                      95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
    100                      105                      110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
    115                      120                      125
Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
    130                      135                      140                      145
Lys Gly Arg Arg Arg Gln
                      150

```

<210> 326  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

```

<400> 326
Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
-15                      -10                      -5                      1
Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
    5                      10                      15
Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
    20                      25                      30
Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr

```

35	40	45
Thr Arg Arg Pro Ala Phe Pro Val Ile His Leu Glu Asp Ile Thr Leu		
50	55	60
Asp Tyr Ser Asp Val Asp Ser Phe Thr Gly Ser Pro Val Ser Met Leu		
70	75	80
Asn Asp Leu Ile Thr Phe Asp Thr Thr Lys Phe Gly Glu Thr Met Thr		
85	90	95
Pro Glu Thr Asn Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Ala Thr		
100	105	110
Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr		
115	120	125
Met Pro Pro Pro Ser Gln Thr Ala Leu Thr His Asn		
130	135	140

<210> 327  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -32...-1

<400> 327
Met Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu
-30 -25 -20
Ser Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys
-15 -10 -5
Leu Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp
1 5 10 15
Ala Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr
20 25 30
Asn Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln
35 40 45
Cys Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro
50 55 60
Cys Cys Cys Asp Ile Asn Glu Gly Leu
65 70

<210> 328  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27...-1

<400> 328
Met Ser Asp Glu Asp Glu Ser Ser Asp Tyr Leu Cys Leu Ser Ile Leu
-25 -20 -15
Gly Leu Phe Cys Cys Leu Pro Leu Ala Ile Pro Ala Val Ile Phe Ser
-10 -5 1 5
Cys Leu Thr Lys Asn Tyr Asn Lys Ser Ser Asp Tyr Glu Leu Ala Ala
10 15 20
Lys Thr Ser Lys Gln Ala Tyr Tyr Trp Ala Ile Ala Ser Ile Thr Val
25 30 35
Gly Ile Leu Gly Thr Ile Leu Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg

40 45 50  
 Leu  
 <210> 329  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -27..-1  
 <400> 329  
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly Ser Leu Thr  
 -25 -20 -15  
 Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val Phe Pro Gln  
 -10 -5 1 5  
 Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys Ile Ser Leu  
 10 15 20  
 Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln Gly Asp Leu  
 25 30 35  
 Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe Ser Ile Ile  
 40 45 50  
 Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val Gly Arg  
 55 60 65  
 <210> 330  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -20..-1  
 <400> 330  
 Met Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His  
 -20 -15 -10 -5  
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly  
 1 5 10  
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys  
 15 20 25  
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser  
 30 35 40  
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn  
 45 50 55 60  
 Thr Val Arg Thr  
 <210> 331  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> SIGNAL  
 <222> -32..-1  
 <400> 331

Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro  
-30 -25 -20  
Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala  
-15 -10 -5  
Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe  
1 5 10 15  
Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys  
20 25 30  
Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro  
35 40 45  
Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met  
50 55 60  
Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp  
65 70 75 80  
Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val  
85 90

<210> 332  
<211> 62  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -46...-1

<400> 332  
Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp  
-45 -40 -35  
Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile  
-30 -25 -20 -15  
Thr Ala Val Leu Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu  
-10 -5 1  
Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu Glu  
5 10 15

<210> 333  
<211> 150  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -23...-1

<400> 333  
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys  
-20 -15 -10  
Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys  
-5 1 5  
Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys  
10 15 20 25  
Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe  
30 35 40  
Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys  
45 50 55  
Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu  
60 65 70

Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr  
75 80 85  
Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro  
90 95 100 105  
Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu  
110 115 120  
Glu Gly Ala Arg Arg Tyr  
125

<210> 334  
<211> 198  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -13...-1

<400> 334  
Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp  
-10 -5 1  
Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg  
5 10 15  
Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala  
20 25 30 35  
Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val  
40 45 50  
Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg  
55 60 65  
Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro  
70 75 80  
Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu  
85 90 95  
Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn  
100 105 110 115  
Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys  
120 125 130  
Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg  
135 140 145  
Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp  
150 155 160  
Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys  
165 170 175  
Ile Tyr Leu Arg Gly Lys  
180 185

<210> 335  
<211> 88  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -24...-1

<400> 335  
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala Leu Glu  
-20 -15 -10

Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly Leu Val  
                   -5                  1                  5  
 Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe Leu Met  
       10                  15                  20  
 Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu Ser Asp  
 25                  30                  35                  40  
 Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val Leu Ile  
                   45                  50                  55  
 Ile Leu Glu Val Leu Gln Phe Gln  
                   60

<210> 336  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -45...-1

<400> 336  
 Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe  
 -45                  -40                  -35                  -30  
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln  
                   -25                  -20                  -15  
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro  
                   -10                  -5                  1  
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly  
       5                  10                  15  
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala  
 20                  25                  30                  35  
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro  
                   40                  45                  50  
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro  
                   55                  60                  65  
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys  
       70                  75                  80  
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu  
       85                  90                  95  
 Asp Val Phe Arg Met Thr  
 100                  105

<210> 337  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 337  
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln  
                   -15                  -10                  -5  
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr  
       1                  5                  10  
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu  
       15                  20                  25

Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu
30					35				40					45	
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr
			50						55					60	
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly
		65						70					75		
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro
		80					85					90			
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser
	95				100						105				
Lys	Leu	Gln	Lys	Phe	Thr	Arg	Ser	Ala	Ser	Cys	Ser	Thr	His		
110					115					120					

<210> 338  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -27..-1

<220>  
 <221> UNSURE  
 <222> 21  
 <223> Xaa = Ala,Pro

Thr	Ser	Glu	Glu	Arg	Thr	Ala	Met	Lys	Arg	Glu	Gly	Gly	Ala	Ala	His
		-25					-20					-15			
Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn	His
	-10				-5					1				5	
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa
			10					15					20		
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser
		25					30					35			
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser
	40					45					50				
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg
	55				60					65					
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg	Val
70					75					80					85

<210> 339  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -32..-1

Met	Pro	Cys	Leu	Asp	Gln	Gln	Leu	Thr	Val	His	Ala	Leu	Pro	Cys	Pro
		-30				-25						-20			
Ala	Gln	Pro	Ser	Ser	Leu	Ala	Phe	Cys	Gln	Val	Gly	Phe	Leu	Thr	Ala
	-15				-10						-5				
Gln	Pro	Ser	Pro	Pro	Arg	Arg	Arg	Asn	Gly	Lys	Asp	Arg	Tyr	Thr	Leu

1                    5                    10                    15  
 Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu  
                   20                    25                    30  
 Val Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His  
                   35                    40                    45  
 Gln Ser Ile Thr Val Ala Asp Thr Asn Lys  
                   50                    55

<210> 340  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -35...-1

<400> 340  
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly  
 -35                    -30                    -25                    -20  
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala  
                   -15                    -10                    -5  
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro  
                   1                    5                    10  
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala  
                   15                    20                    25  
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys  
 30                    35                    40                    45

<210> 341  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 341  
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly Phe Leu Tyr  
 -15                    -10                    -5                    1  
 Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe Pro Pro Arg  
                   5                    10                    15  
 Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly Glu Pro Thr  
                   20                    25                    30  
 Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr Ile Glu Trp  
                   35                    40                    45  
 Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp Pro Arg Ser  
 50                    55                    60                    65  
 His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu Arg Ile Val  
                   70                    75                    80  
 His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val Cys Val Ala  
                   85                    90                    95  
 Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser Leu Glu Val  
                   100                    105                    110  
 Ala Cys Lys  
 115

<210> 342  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -39...-1

<400> 342  
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser  
                   -35                  -30                  -25  
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly  
                   -20                  -15                  -10  
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn  
                   -5                  1                  5  
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala  
 10                  15                  20                  25  
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala  
                   30                  35                  40  
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu  
                   45                  50                  55  
 Leu Leu Leu  
                   60

<210> 343  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -43...-1

<400> 343  
 Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile  
                   -40                  -35                  -30  
 Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly  
                   -25                  -20                  -15  
 Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val  
                   -10                  -5                  1                  5  
 Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu  
                   10                  15                  20  
 Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser  
                   25                  30                  35  
 Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys  
                   40                  45                  50  
 Arg Tyr  
                   55

<210> 344  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<220>  
 <221> UNSURE  
 <222> 185  
 <223> Xaa = Phe,Val

<400> 344  
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu  
                           -15                          -10                          -5  
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser  
                           1                          5                          10  
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala  
           15                          20                          25  
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His  
 30                          35                          40                          45  
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu  
                           50                          55                          60  
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu  
                           65                          70                          75  
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp  
                           80                          85                          90  
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser  
           95                          100                          105  
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly  
 110                          115                          120                          125  
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His  
                           130                          135                          140  
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu  
                           145                          150                          155  
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser  
           160                          165                          170  
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys  
           175                          180                          185  
 Phe Gly Gly Asp Arg Leu Thr Leu His  
 190                          195

<210> 345  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -20..-1

<400> 345  
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro  
 -20                          -15                          -10                          -5  
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile  
                           1                          5                          10  
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val  
           15                          20                          25  
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val  
           30                          35                          40  
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr  
 45                          50                          55                          60  
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu  
                           65                          70                          75

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val  
80 85 90  
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn  
95 100 105  
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser  
110 115 120  
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala  
125 130 135 140  
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe  
145 150 155  
Asp Arg His Lys Met Leu Ser  
160

<210> 346  
<211> 247  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -13...-1

<400> 346  
Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr  
-10 -5 1  
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr  
5 10 15  
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys  
20 25 30 35  
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr  
40 45 50  
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg  
55 60 65  
Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg  
70 75 80  
Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln  
85 90 95  
Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile  
100 105 110 115  
Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly  
120 125 130  
Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu  
135 140 145  
Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly  
150 155 160  
Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn  
165 170 175  
Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala  
180 185 190 195  
Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg  
200 205 210  
Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn Met Leu Leu Ile Pro  
215 220 225  
Thr Ser Phe Ser Pro Leu Lys  
230

<210> 347  
<211> 104

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -47..-1

<400> 347  
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro  
           -45                  -40                  -35  
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp  
       -30                  -25                  -20  
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn  
 -15                  -10                  -5                  1  
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr  
           5                  10                  15  
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp  
       20                  25                  30  
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu  
       35                  40                  45  
 Gly Leu Ala Phe Gln Cys Arg Phe  
 50                  55

<210> 348  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21..-1

<400> 348  
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val  
       -20                  -15                  -10  
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg  
 -5                  1                  5                  10  
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala  
       15                  20                  25  
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn  
       30                  35                  40  
 Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu  
       45                  50                  55  
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser  
 60                  65                  70                  75  
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln  
       80                  85                  90  
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr  
       95                  100

<210> 349  
 <211> 302  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -18..-1

<400> 349

Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu Ala Val Asn Val Val  
-15 -10 -5  
Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr Ala Thr Glu Glu Ala  
1 5 10  
Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly Leu Phe Ile Tyr Gln  
15 20 25 30  
Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg Arg Thr Asn Ser Cys  
35 40 45  
Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys Asp Ser Leu Ser Thr  
50 55 60  
Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala Arg Leu Gly Thr Tyr  
65 70 75  
Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly Met Phe Val Phe Tyr  
80 85 90  
Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met Leu Arg Phe Gly Lys  
95 100 105 110  
Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val Ile Val Phe Val Leu  
115 120 125  
Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr Thr Gly Thr Ser Val  
130 135 140  
Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile Ile Leu Ala Ile Met  
145 150 155  
Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu Lys His Pro Cys Leu  
160 165 170  
Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys Val Ser Gln Lys Leu  
175 180 185 190  
Val Val Ala His Met Thr Lys Ser Glu Leu Tyr Leu Gln Asp Thr Val  
195 200 205  
Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln Tyr Phe Asn Asn Phe  
210 215 220  
Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met Val Ile Ser Ser Phe  
225 230 235  
Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu Gln Ile Ser Arg His  
240 245 250  
Leu His Leu Asn Ile Phe Lys Thr Ala Cys His Gln Ala Pro Glu Gln  
255 260 265 270  
Val Gln Val Leu Ser Ser Lys Ser His Gln Asn Asn Met Asp  
275 280

<210> 350

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 350

Met Ile Leu Val Thr Val Pro Gly Val Cys Pro Ala Gln Cys Cys Trp  
-10 -5 1  
Ala Glu Gln Arg Gly Arg Gly Ser Gly Met Tyr Phe Ile Asp Lys Trp  
5 10 15  
Ala Arg Pro Ser Trp Val Pro His Trp Leu Asn Asp Leu Phe Ile Val  
20 25 30  
Lys Ser Gly Tyr Leu Val Cys Ile Arg Thr Thr Val Ile Arg Gln Gly

35                      40                      45                      50  
 Ile Val Arg Ile Gly Arg Asn Lys Ile Ser Glu Ser Gly Arg Ser Ala  
                          55                      60                      65  
 Leu Tyr Thr Ile Ala Lys Asn Lys Met Val Ile Phe Lys Val Pro Asp  
                          70                      75                      80  
 Cys Met His Leu Asn Ala Asp Tyr Phe Gly Val  
                          85                      90

<210> 351  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 351  
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser  
                          -30                      -25                      -20  
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala  
                          -15                      -10                      -5  
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr  
                          1                      5                      10  
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe  
 15                      20                      25                      30  
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val  
                          35                      40                      45  
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser  
                          50                      55                      60  
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val  
                          65                      70                      75  
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe  
                          80                      85                      90  
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln  
 95                      100                      105                      110  
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr  
                          115                      120                      125  
 Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly  
                          130                      135                      140  
 Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln  
                          145                      150                      155  
 Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn  
                          160                      165                      170  
 Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu  
 175                      180                      185                      190  
 Ala Ser Glu Lys Lys  
                          195

<210> 352  
 <211> 206  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -34...-1

<400> 352  
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser  
-30 -25 -20  
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala  
-15 -10 -5  
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr  
1 5 10  
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe  
15 20 25 30  
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val  
35 40 45  
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser  
50 55 60  
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val  
65 70 75  
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe  
80 85 90  
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln  
95 100 105 110  
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr  
115 120 125  
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly  
130 135 140  
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg  
145 150 155  
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys  
160 165 170

<210> 353  
<211> 88  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -44...-1

<400> 353  
Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp Gly Arg Arg Cys  
-40 -35 -30  
Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro  
-25 -20 -15  
Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp  
-10 -5 1  
Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr  
5 10 15 20  
Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser Arg Ala Ala Leu  
25 30 35  
Cys Ser Arg Ala Ser Thr Tyr Val  
40

<210> 354  
<211> 151  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL

<222> -32..-1

<400> 354

Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg  
-30 -25 -20  
His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser  
-15 -10 -5  
Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu  
1 5 10 15  
Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser  
20 25 30  
Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp  
35 40 45  
Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala  
50 55 60  
Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile  
65 70 75 80  
Asp Gly Lys Ala Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr  
85 90 95  
Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp  
100 105 110  
Arg Leu Lys Gln Gly Lys Phe  
115

<210> 355

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16..-1

<400> 355

Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala  
-15 -10 -5  
Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly  
1 5 10 15  
His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser  
20 25 30  
Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr  
35 40 45  
Leu

<210> 356

<211> 189

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24..-1

<220>

<221> UNSURE

<222> 41

<223> Xaa = Ala,Gly

<400> 356

```
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
      -20      -15      -10
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
      -5      1      5
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
      10      15      20
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
      25      30      35      40
Xaa Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
      45      50      55
Leu Thr Phe Trp Gly Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
      60      65      70
Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
      75      80      85
Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
      90      95      100
Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
      105      110      115      120
Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
      125      130      135
His Gly Leu Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
      140      145      150
Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
      155      160      165
```

<210> 357

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47..-1

<400> 357

```
Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro Phe Ala Phe Glu
      -45      -40      -35
Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser Leu Ser Asp Pro
      -30      -25      -20
Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met Ala Leu Cys Ala
      -15      -10      -5      1
Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys Lys Leu Ile Leu
      5      10      15
Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile Val Ala Leu Leu
      20      25      30
Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser Lys Glu Gln Gln
      35      40      45
Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Gly Gly Val
      50      55      60      65
Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser Ser Asp Ser Ser
      70      75      80
Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr Arg His His Ala
      85      90      95
Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser Pro Tyr Trp Pro
      100      105      110
Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
      115      120      125
```

Lys Val Leu Gly Leu Pro Ala  
130 135

<210> 358  
<211> 102  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14..-1

<400> 358  
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln  
-10 -5 1  
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys  
5 10 15  
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp  
20 25 30  
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala  
35 40 45 50  
Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser  
55 60 65  
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn  
70 75 80  
Val Thr Lys Lys Trp Ser  
85

<210> 359  
<211> 244  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -29..-1

<400> 359  
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala Ile Tyr Ile Leu Thr  
-25 -20 -15  
Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu Trp Ser Trp Ile Cys  
-10 -5 1  
Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn  
5 10 15  
Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu  
20 25 30 35  
Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Glu Val Gly Cys Gly  
40 45 50  
Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys  
55 60 65  
Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala  
70 75 80  
Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu  
85 90 95  
Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Val Cys Thr  
100 105 110 115  
Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val  
120 125 130

Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val  
                   135                  140                  145  
 Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp  
                   150                  155                  160  
 Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser  
                   165                  170                  175  
 Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His  
 180                  185                  190                  195  
 Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg Pro His Ile Tyr Gly  
                   200                  205                  210  
 Tyr Ala Val Lys  
                   215

<210> 360  
 <211> 177  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 360  
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys  
                   -20                  -15                  -10  
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys  
                   -5                  1                  5  
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys  
 10                  15                  20                  25  
 Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys Cys  
                   30                  35                  40  
 Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile Tyr  
                   45                  50                  55  
 Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val His  
                   60                  65                  70  
 Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys Gln  
                   75                  80                  85  
 Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile Asn  
 90                  95                  100                  105  
 Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val Ile  
                   110                  115                  120  
 Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys Ile  
                   125                  130                  135  
 Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg Arg  
                   140                  145                  150  
 Tyr

<210> 361  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -21...-1

<400> 361  
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala

-20						-15						-10				
Pro	Pro	Thr	Val	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Phe	Pro	Ala	Ala	Gln	
-5					1				5					10		
Met	Met	Asn	Asn	Gly	Leu	Leu	Gln	Gln	Pro	Ser	Ala	Leu	Met	Leu	Leu	
		15						20					25			
Pro	Cys	Arg	Pro	Val	Leu	Thr	Ser	Val	Ala	Leu	Asn	Ala	Asn	Phe	Val	
	30						35					40				
Ser	Trp	Lys	Ser	Arg	Thr	Lys	Tyr	Thr	Ile	Thr	Pro	Val	Lys	Met	Arg	
45						50					55					
Lys	Ser	Gly	Gly	Arg	Asp	His	Thr	Gly	Ala	Gly	Asn	Val	Arg	Arg	Thr	
60					65					70					75	
Val	Gly	Arg	Val	Ser	Asn	Val	Asp	His	Asn	Lys	Arg	Val	Ile	Gly	Lys	
				80					85					90		
Ala	Gly	Arg	Asn	Arg	Trp	Leu	Gly	Lys	Arg	Pro	Asn	Ser	Gly	Arg	Trp	
			95					100					105			
His	Arg	Lys	Gly	Gly	Trp	Ala	Gly	Arg	Lys	Ile	Arg	Pro	Leu	Pro	Pro	
		110					115					120				
Met	Lys	Ser	Tyr	Val	Lys	Leu	Pro	Ser	Ala	Ser	Ala	Gln	Ser			
125						130					135					

<210> 362  
 <211> 186  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 362																
Met	Ala	Thr	Ala	Ser	Pro	Ser	Val	Phe	Leu	Leu	Met	Val	Asn	Gly	Gln	
				-15				-10					-5			
Val	Glu	Ser	Ala	Gln	Phe	Pro	Glu	Tyr	Asp	Asp	Leu	Tyr	Cys	Lys	Tyr	
		1					5					10				
Cys	Phe	Val	Tyr	Gly	Gln	Asp	Trp	Ala	Pro	Thr	Ala	Gly	Leu	Glu	Glu	
	15				20						25					
Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu	
30				35					40					45		
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr	
		50						55					60			
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly	
		65					70					75				
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro	
	80					85					90					
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser	
	95				100						105					
Lys	Leu	Gln	Lys	Phe	Thr	Ser	Trp	Phe	Met	Gly	Arg	Arg	Pro	Glu	Tyr	
110				115						120				125		
Thr	Asp	Pro	Lys	Val	Val	Ala	Gln	Gly	Glu	Gly	Arg	Glu	Ala	Ile	Thr	
			130					135						140		
Ala	Pro	Arg	Lys	Ala	Val	Phe	Ser	Val	His	Gly	Leu	Thr	Ser	Pro	Arg	
		145					150					155				
Ala	Leu	Ala	Leu	Val	His	Ile	Lys	Gly	Thr							
160						165										

<210> 363  
 <211> 150  
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47..-1

<400> 363

```
Met Gly Asp Arg Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro
      -45                      -40                      -35
Trp Pro His Thr Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln
      -30                      -25                      -20
Pro Thr Ala Leu Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val
      -15                      -10                      -5                      1
Gly Ser Ala Pro Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
      5                      10                      15
Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
      20                      25                      30
Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
      35                      40                      45
Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
      50                      55                      60                      65
Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
      70                      75                      80
Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
      85                      90                      95
Pro Gly Ile His Leu Cys
      100
```

<210> 364

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45..-1

<400> 364

```
Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu Leu His Leu
      -45                      -40                      -35                      -30
Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser Val Ser Ala
      -25                      -20                      -15
Phe Ile Leu Leu Leu Leu Leu Ser Gly Pro Ala Glu Met Ser Ala Ser
      -10                      -5                      1
Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala Ser Leu Ile
      5                      10                      15
Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser Thr Leu Leu
      20                      25                      30                      35
Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val Asn Leu
      40                      45                      50
```

<210> 365

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 365

Met	Ala	Ala	Ile	Glu	Ile	Glu	Val	Lys	Pro	Asn	Gln	Gly	Phe	Cys	Gly
-25						-20					-15				
Ser	Ala	Cys	Leu	Leu	Ala	Val	Ile	Arg	Ala	Phe	Phe	Phe	Lys	Lys	Asn
-10					-5				1					5	
Ala	Cys	Leu	Leu	Arg	Glu	Ile	Leu	Gln	Ser	Lys	Leu	Gly	Gly	Met	Gly
		10					15						20		
Pro	Val	Val	Phe	Ser	Tyr	Arg	Gly	Leu	Pro	Leu	Trp	Leu	Phe	Ala	Trp
	25						30					35			
Leu	Phe	Pro	Arg	Cys	Thr	Val	Pro	Leu	Thr	Phe	Gly	Phe	Glu	Asn	Met
40					45						50				
Arg	Gly	Leu	Gly	Val	Val	Ala	Tyr	Ala	Cys	Asn	Pro	Ser	Thr		
55					60					65					

<210> 366

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -40...-1

<400> 366

Met	Thr	Ser	Met	Thr	Gln	Ser	Leu	Arg	Glu	Val	Ile	Lys	Ala	Met	Thr
-40					-35					-30				-25	
Lys	Ala	Arg	Asn	Phe	Glu	Arg	Val	Leu	Gly	Lys	Ile	Thr	Leu	Val	Ser
			-20						-15					-10	
Ala	Ala	Pro	Gly	Lys	Val	Ile	Cys	Glu	Met	Lys	Val	Glu	Glu	Glu	His
			-5				1				5				
Thr	Asn	Ala	Ile	Gly	Thr	Leu	His	Gly	Gly	Leu	Thr	Ala	Thr	Leu	Val
10						15				20					
Asp	Asn	Ile	Ser	Thr	Met	Ala	Leu	Leu	Cys	Thr	Glu	Arg	Gly	Ala	Pro
25					30					35				40	
Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr	Tyr	Met	Ser	Pro	Ala	Lys	Leu
			45						50					55	
Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His	Val	Leu	Lys	Gln	Gly	Lys	Thr
		60					65					70			
Leu	Ala	Phe	Thr	Ser	Val	Asp	Leu	Thr	Asn	Lys	Ala	Thr	Gly	Lys	Leu
	75					80						85			
Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His	Leu	Gly	Asn				
90						95					100				

<210> 367

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 367

Met	Asp	Pro	Gly	Trp	Pro	His	Phe	Lys	Leu	Thr	His	Ser	Arg	Cys	Met
-35					-30					-25				-20	
Ala	Val	Leu	Phe	Leu	Gly	Thr	Leu	Pro	Leu	Cys	Pro	Val	Thr	Ser	Pro

Val Trp Gly Trp Ser Pro Gly  
1

-15

-10

-5

<210> 368  
<211> 78  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -41..-1

<400> 368  
Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr  
-40 -35 -30  
Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu  
-25 -20 -15 -10  
Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val  
-5 1 5  
Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val  
10 15 20  
Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly  
25 30 35

<210> 369  
<211> 83  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -40..-1

<400> 369  
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly  
-40 -35 -30 -25  
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val  
-20 -15 -10  
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu  
-5 1 5  
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu  
10 15 20  
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn  
25 30 35 40  
Lys Ser Lys

<210> 370  
<211> 92  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -15..-1

<400> 370  
Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala

```

-15          -10          -5          1
Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro Arg Ala Trp Leu Gly Phe
      5          10          15
Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln Gln Ala Arg Gly Lys Ala
      20          25          30
Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile Lys Arg Lys Asn Lys His
      35          40          45
Gly Trp Val Arg Arg Leu Ser Thr Pro Ala Gly Val Gln Val Ile Leu
50          55          60          65
Arg Arg Met Leu Lys Gly Arg Lys Ser Leu Ser His
      70          75

```

```

<210> 371
<211> 279
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> -42..-1

```

```

<400> 371
Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly Gly Trp
      -40          -35          -30
Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg Ser Leu
      -25          -20          -15
Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg Leu Leu
-10          -5          1          5
Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro Leu Thr
      10          15          20
Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu Ile Glu
      25          30          35
Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu Asn Gln
      40          45          50
Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp Glu Gln
55          60          65          70
Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln Lys Phe
      75          80          85
Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu Lys Asn
      90          95          100
Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val Leu Leu
      105          110          115
Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro Gln Ala
      120          125          130
Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg Thr Leu
135          140          145          150
Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly Asn Ala
      155          160          165
Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg Thr Glu
      170          175          180
Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu Leu Leu Thr
      185          190          195
Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp Val Ile
      200          205          210
Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala Gln Val
215          220          225          230
Arg Arg Phe Val Ser Asp Leu
      235

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<210> 372  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 372  
 Met Ala Cys Thr Thr Thr Ala Pro Ala Gln Glu His Met Leu Leu Thr  
 -30 -25 -20  
 Pro Leu Thr Ala Leu Met Val Gly Ala Ala Ser Leu Leu Glu Gly Arg  
 -15 -10 -5 1  
 Pro Gln Ile Ser Ala Pro Tyr Ser Arg Ala Ala Cys Cys Ser Pro Gly  
 5 10 15  
 Ala Leu Gly Cys Pro Ala Ala Arg Val Gly Ile Leu Asp Leu Met Tyr  
 20 25 30  
 Ser Trp Val Ala Arg Lys Val Leu Arg Cys Ser Asn Thr Gly Leu Gln  
 35 40 45  
 Gly Leu His Cys Ala Pro Ala Tyr Ala Ala Gln Leu Gly Met Asp Pro  
 50 55 60 65  
 Gly Arg Gly Gln Arg Ala Gly Gly Pro Val Glu Gln Thr Tyr Phe Ser  
 70 75 80  
 Pro Met Gly Lys Leu Pro Thr Leu Ser Trp Leu Glu Gly Cys Thr Ala  
 85 90 95  
 Val Met Thr Leu Ala Ser Ala Trp Leu Leu Gly Ser Pro Arg Glu Thr  
 100 105 110  
 Tyr Asn His Glu Lys Val Lys Glu Lys Gln Cys Pro Phe Ser Ser Met  
 115 120 125  
 Val Leu Gly Glu Tyr Gly Phe Leu Pro Thr Val Asp His Leu Ser Thr  
 130 135 140 145  
 Leu Gly Cys Asn Met Arg Glu Leu  
 150

<210> 373  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -42...-1

<400> 373  
 Met Ala His Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys  
 -40 -35 -30  
 Ile Pro Gly Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys  
 -25 -20 -15  
 Phe His Leu Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr  
 -10 -5 1 5  
 Ala Pro Val Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu  
 10 15 20  
 Asp Leu Val Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val  
 25 30 35  
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala  
 40 45 50

Cys Thr His Arg Asp  
55

<210> 374  
<211> 85  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20..-1

<400> 374  
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser  
-20 -15 -10 -5  
Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu  
1 5 10  
Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln  
15 20 25  
Gln Pro Cys Lys Ser Gly Gly Gly Val Gly Glu Pro Asn Ala Gln  
30 35 40  
Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser  
45 50 55 60  
His Gly Gln Ala Phe  
65

<210> 375  
<211> 90  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -28..-1

<400> 375  
Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val  
-25 -20 -15  
Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys  
-10 -5 1  
Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val  
5 10 15 20  
Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe  
25 30 35  
Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg  
40 45 50  
Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly  
55 60

<210> 376  
<211> 89  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -33..-1

<220>  
 <221> UNSURE  
 <222> 47  
 <223> Xaa = Ala,Pro,Ser,Thr

<400> 376  
 Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu  
                   -30                  -25                  -20  
 Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser  
                   -15                  -10                  -5  
 Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu  
       1                  5                  10                  15  
 Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala  
                   20                  25                  30  
 Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa  
                   35                  40                  45  
 Gly Pro Leu Ile Pro Gly Gln Cys Pro  
           50                  55

<210> 377  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -15...-1

<400> 377  
 Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu  
 -15                  -10                  -5                  1  
 Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser  
           5                  10                  15  
 Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg  
           20                  25                  30  
 Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val  
       35                  40                  45  
 Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu  
   50                  55                  60                  65  
 Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg  
                   70                  75                  80  
 Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val  
           85                  90                  95  
 Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr  
           100                  105                  110  
 Arg Ala Arg Thr  
       115

<210> 378  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<220>

<221> UNSURE  
 <222> 50  
 <223> Xaa = Ala,Gly

<220>  
 <221> UNSURE  
 <222> 51  
 <223> Xaa = Leu,Met,Val

<400> 378  
 Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln  
                   -10                  -5                  1  
 Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys  
           5                  10                  15  
 Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp  
       20                  25                  30  
 Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa  
 35                  40                  45                  50  
 Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser  
                   55                  60                  65  
 Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn  
           70                  75                  80  
 Val Thr Lys Lys Trp Ser  
           85

<210> 379  
 <211> 504  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -24..-1

<400> 379  
 Met Gly Ile Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser  
                   -20                  -15                  -10  
 Leu Val Leu Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu  
           -5                  1                  5  
 Ala Ser Gln Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg  
       10                  15                  20  
 Pro Gly Trp Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu  
 25                  30                  35                  40  
 Trp Val Met Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu  
           45                  50                  55  
 Ser Gly His Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys  
       60                  65                  70  
 Leu Arg Ser Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly  
       75                  80                  85  
 Thr Met Gly Pro Trp Tyr Leu Leu Leu Leu Leu Gly His Cys Val Gly  
       90                  95                  100  
 Leu Tyr Val Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu  
 105                  110                  115                  120  
 Gly Leu Ala Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp  
           125                  130                  135  
 Gln Ser Gly Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe  
           140                  145                  150  
 His Gly Gly Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu

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 475  
 480

Glu	Ser	Cys	Ala	His	Pro	Asp	Arg	His	Tyr	Ser	Leu	Ala	Asp	Leu	Leu
170						175					180				
Lys	Tyr	Ser	Phe	Tyr	Leu	Pro	Phe	Phe	Phe	Phe	Gly	Pro	Ile	Met	Thr
185					190					195					200
Phe	Asp	Arg	Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg
				205					210					215	
Glu	Gly	Glu	Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val
			220					225					230		
Ala	Ile	Met	Ala	Val	Asp	Ile	Phe	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr
	235						240					245			
Ile	Pro	Ser	Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu
	250					255					260				
Ala	Gly	Leu	Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala
265					270					275					280
Val	Leu	Phe	Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp
				285					290					295	
Pro	Pro	Gln	Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu
			300					305					310		
Thr	His	Phe	Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr
		315					320					325			
Asn	His	Ile	Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala
	330					335					340				
Thr	Val	Ala	Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp
345					350					355					360
Ile	Val	Tyr	Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu
			365						370					375	
Leu	Trp	Met	Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu
			380					385					390		
Ala	Ser	Leu	Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly
	395						400					405			
Ala	Met	Asn	Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn
	410					415					420				
Ser	Leu	Lys	Phe	Thr	Glu	Leu	Val	Ala	Arg	Arg	Leu	Leu	Leu	Thr	Gly
425					430				435						440
Phe	Pro	Gln	Thr	Thr	Leu	Ser	Ile	Leu	Phe	Val	Thr	Tyr	Cys	Gly	Val
			445						450					455	
Gln	Leu	Val	Lys	Glu	Arg	Glu	Arg	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Gln
		460						465					470		
Lys	Gln	Asp	Lys	Glu	Lys	Pro	Glu								
	475					480									

<210> 380  
 <211> 152  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26..-1

<400> 380  
 Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe Cys Val  
 -25 -20 -15  
 Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly Tyr Ala  
 -10 -5 1 5  
 Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser Ala His  
 10 15 20

Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro  
           25                          30                          35  
 Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu  
           40                          45                          50  
 Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys  
 55                          60                          65                          70  
 Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser  
                           75                          80                          85  
 Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser  
                           90                          95                          100  
 Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala  
           105                          110                          115  
 Thr Leu Leu Ile Leu Asp Ile Trp  
           120                          125

<210> 381  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -26...-1

<400> 381  
 Met Glu Met Leu Phe Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe  
           -25                          -20                          -15  
 Lys Phe Ser Leu Cys Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe  
           -10                          -5                          1                          5  
 Gly Ser Val Ala Cys Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly  
                           10                          15                          20  
 Ser Arg Leu  
           25

<210> 382  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -23...-1

<400> 382  
 Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu  
           -20                          -15                          -10  
 Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg  
           -5                          1                          5  
 Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly  
 10                          15                          20                          25  
 Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys  
                           30                          35                          40  
 Val Tyr Lys Pro Ile Arg Arg Arg  
           45

<210> 383  
 <211> 95  
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48..-1

<400> 383

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Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
      -45                      -40                      -35
Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
      -30                      -25                      -20
Thr Ala Cys Phe Val Ile Leu Leu Phe Ile Phe Thr Val Val Ser
      -15                      -10                      -5
Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys
1          5          10          15
Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
      20          25          30
Arg Ser Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
      35          40          45
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<210> 384

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 384

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Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
-20                      -15                      -10                      -5
Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
      1          5          10
Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
      15          20          25
Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
      30          35          40
Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
      45          50          55          60
Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe
      65          70          75
Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
      80          85          90
Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala Pro
      95          100          105
Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met Ala
      110          115          120
Ser Met Glu Ser Pro Gln
125          130
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<210> 385

<211> 354

<212> PRT

<213> Homo sapiens

<400> 385

Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro

1				5				10					15				
Met	Pro	Thr	Cys	Arg	Val	Tyr	Gly	Thr	Val	Ala	His	Gln	Asp	Gly	His		
			20					25					30				
Leu	Leu	Val	Leu	Gly	Gly	Cys	Gly	Arg	Ala	Gly	Leu	Pro	Leu	Asp	Thr		
		35					40					45					
Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro		
	50					55					60						
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln		
65					70					75					80		
Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala		
				85				90						95			
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr		
		100					105					110					
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met		
	115					120					125						
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln		
130					135					140							
Val	Arg	Val	Tyr	Asp	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser		
145				150				155						160			
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys		
				165				170						175			
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe		
		180					185						190				
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu		
	195					200					205						
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val		
	210				215					220							
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser		
225				230				235						240			
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly		
			245					250					255				
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala		
	260						265					270					
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly		
	275					280					285						
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu		
	290				295					300							
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys		
305				310						315					320		
Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly		
			325					330						335			
Val	Ala	Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp		
		340					345					350					

<210> 386  
 <211> 207  
 <212> PRT  
 <213> Homo sapiens

<400> 386  
 Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala  
 1 5 10 15  
 Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe  
 20 25 30  
 Lys Leu Glu Gly Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp  
 35 40 45  
 Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val

50 55 60  
 Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp  
 65 70 75 80  
 Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val Thr Val Lys Arg  
 85 90 95  
 Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp Met Ser Arg Asp  
 100 105 110  
 Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe Thr Tyr Ala Gln  
 115 120 125  
 Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala Pro Val Glu Gly  
 130 135 140  
 Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu Tyr Glu Ala Gln  
 145 150 155 160  
 Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val Val His Thr Leu  
 165 170 175  
 Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe Ala Leu Trp Asp  
 180 185 190  
 Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro Glu Gly Leu  
 195 200 205

<210> 387  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 387  
 Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly  
 1 5 10 15  
 Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg  
 20 25 30  
 Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp  
 35 40 45  
 Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala  
 50 55 60  
 Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala  
 65 70 75 80  
 Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val  
 85 90 95  
 Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu  
 100 105 110  
 Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu  
 115 120 125  
 Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala  
 130 135 140  
 Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp  
 145 150 155 160  
 Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro  
 165 170 175  
 Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu  
 180 185 190  
 Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly  
 195 200 205  
 Leu Gln  
 210

<210> 388  
 <211> 375  
 <212> PRT

<213> Homo sapiens

<400> 388

Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu  
1 5 10 15  
Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln  
20 25 30  
Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu  
35 40 45  
Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser  
50 55 60  
Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu  
65 70 75 80  
Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys  
85 90 95  
Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Pro Gln Phe Tyr Ser  
100 105 110  
Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr  
115 120 125  
Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser  
130 135 140  
Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala  
145 150 155 160  
Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser  
165 170 175  
Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala  
180 185 190  
Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp  
195 200 205  
Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr  
210 215 220  
Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val  
225 230 235 240  
Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala  
245 250 255  
Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His  
260 265 270  
Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu  
275 280 285  
Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr  
290 295 300  
Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro  
305 310 315 320  
Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile  
325 330 335  
Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe  
340 345 350  
Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu  
355 360 365  
Lys Met Ser Gly Arg Lys His  
370 375

<210> 389

<211> 509

<212> PRT

<213> Homo sapiens

<400> 389

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500

Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys Val Ala  
 1 5 10 15  
 Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala Gly Asp  
 20 25 30  
 Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu Ile Val  
 35 40 45  
 Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn Thr Val  
 50 55 60  
 Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro Gln Ala  
 65 70 75 80  
 Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys Asn Gly  
 85 90 95  
 Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe Val Asn  
 100 105 110  
 Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu Thr Ala  
 115 120 125  
 His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr Val Pro  
 130 135 140  
 Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala Ala Arg  
 145 150 155 160  
 Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser Ala Ala  
 165 170 175  
 Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys Ser Asn  
 180 185 190  
 Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser Val Met  
 195 200 205  
 Glu Val Asn Ser Gly Ile Tyr Arg Val Leu Ser Thr Asn Thr Asp Asp  
 210 215 220  
 Asn Ile Gly Gly Ala His Phe Thr Glu Thr Leu Ala Gln Tyr Leu Ala  
 225 230 235 240  
 Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn Ala Arg  
 245 250 255  
 Ala Met Met Lys Leu Thr Asn Ser Ala Glu Val Ala Lys His Ser Leu  
 260 265 270  
 Ser Thr Leu Gly Ser Ala Asn Cys Phe Leu Asp Ser Leu Tyr Glu Gly  
 275 280 285  
 Gln Asp Phe Asp Cys Asn Val Ser Arg Ala Arg Phe Glu Leu Leu Cys  
 290 295 300  
 Ser Pro Leu Phe Asn Lys Cys Ile Glu Ala Ile Arg Gly Leu Leu Asp  
 305 310 315 320  
 Gln Asn Gly Phe Thr Thr Asp Asp Ile Asn Lys Val Val Leu Cys Gly  
 325 330 335  
 Gly Ser Ser Arg Ile Pro Lys Leu Gln Gln Leu Ile Lys Asp Leu Phe  
 340 345 350  
 Pro Ala Val Glu Leu Leu Asn Ser Ile Pro Pro Asp Glu Val Ile Pro  
 355 360 365  
 Ile Gly Ala Ala Ile Glu Ala Gly Ile Leu Ile Gly Lys Glu Asn Leu  
 370 375 380  
 Leu Val Glu Asp Ser Leu Met Ile Glu Cys Ser Ala Arg Asp Ile Leu  
 385 390 395 400  
 Val Lys Gly Val Asp Glu Ser Gly Ala Ser Arg Phe Thr Val Leu Phe  
 405 410 415  
 Pro Ser Gly Thr Pro Leu Pro Ala Arg Arg Gln His Thr Leu Gln Ala  
 420 425 430  
 Pro Gly Ser Ile Ser Ser Val Cys Leu Glu Leu Tyr Glu Ser Asp Gly  
 435 440 445  
 Lys Asn Ser Ala Lys Glu Glu Thr Lys Phe Ala Gln Val Val Leu Gln  
 450 455 460

Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu  
 465 470 475 480  
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu  
 485 490 495  
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser  
 500 505

<210> 390  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens

<400> 390  
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His  
 1 5 10 15  
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu  
 20 25 30  
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His  
 35 40 45  
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu  
 50 55 60  
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr  
 65 70 75

<210> 391  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens

<400> 391  
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val  
 1 5 10 15  
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val  
 20 25 30  
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu  
 35 40 45  
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys  
 50 55 60  
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala  
 65 70 75 80  
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met  
 85 90 95  
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu  
 100 105 110  
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile  
 115 120 125  
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile  
 130 135 140  
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu  
 145 150 155 160  
 Leu Gly

<210> 392  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu  
1 5 10 15  
Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala  
20 25 30  
Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro  
35 40 45  
Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr  
50 55 60  
Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro  
65 70 75 80  
His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val  
85 90 95  
Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys  
100 105 110  
Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu  
115 120 125  
Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu  
130 135 140  
Gly Phe  
145

<210> 393  
<211> 225  
<212> PRT  
<213> Homo sapiens

<400> 393  
Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val  
1 5 10 15  
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val  
20 25 30  
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu  
35 40 45  
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys  
50 55 60  
Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala  
65 70 75 80  
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met  
85 90 95  
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu  
100 105 110  
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile  
115 120 125  
Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile  
130 135 140  
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu  
145 150 155 160  
Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile  
165 170 175  
Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser  
180 185 190  
Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser  
195 200 205  
Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr  
210 215 220  
Val  
225

<210> 394  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 394  
 Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met  
 1 5 10 15  
 Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile  
 20 25 30  
 Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His  
 35 40 45  
 Met Ser Phe His Tyr Thr Val Leu Met Phe Ser Gln Val Ile Ser  
 50 55 60  
 Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn  
 65 70 75 80  
 Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser  
 85 90 95  
 Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu  
 100 105 110  
 Gln Gly

<210> 395  
 <211> 367  
 <212> PRT  
 <213> Homo sapiens

<400> 395  
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro  
 1 5 10 15  
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp  
 20 25 30  
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val  
 35 40 45  
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val  
 50 55 60  
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro  
 65 70 75 80  
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu  
 85 90 95  
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp  
 100 105 110  
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val  
 115 120 125  
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln  
 130 135 140  
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly  
 145 150 155 160  
 Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr  
 165 170 175  
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu  
 180 185 190  
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu  
 195 200 205  
 Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val  
 210 215 220  
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln  
 225 230 235 240



275

<210> 397  
 <211> 173  
 <212> PRT  
 <213> Homo sapiens

<400> 397  
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val  
 1 5 10 15  
 Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly  
 20 25 30  
 Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile  
 35 40 45  
 Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly  
 50 55 60  
 Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val  
 65 70 75 80  
 Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu  
 85 90 95  
 Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile  
 100 105 110  
 Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met  
 115 120 125  
 Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn  
 130 135 140  
 Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly  
 145 150 155 160  
 Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp  
 165 170

<210> 398  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 398  
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser  
 1 5 10 15  
 Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala  
 20 25 30  
 Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala  
 35 40 45  
 Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly  
 50 55 60  
 Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly Leu Arg Pro Leu  
 65 70 75 80  
 Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln Gln Glu Leu Asp  
 85 90 95  
 Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln  
 100 105 110  
 Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln  
 115 120 125  
 Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg  
 130 135 140  
 Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr  
 145 150 155 160  
 Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln

Phe Lys Glu Ile 165 Gln Lys Leu Ile Lys 170 Glu Pro Ala Pro Asp 175 Ser Gly  
 180 185 190  
 Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu His  
 195 200 205

<210> 399  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 399  
 Met Trp Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr  
 1 5 10 15  
 Lys Pro Met Phe Val Ile Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe  
 20 25 30  
 Leu Ala Lys Phe Leu Lys Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala  
 35 40 45  
 Cys Leu Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn  
 50 55 60  
 Thr Ile Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg  
 65 70 75 80  
 Cys Phe Pro Asp Gly Leu Ala His Ser Asp Leu Met Cys Thr Gly Asp  
 85 90 95  
 Lys Asp Val Val Asn Glu Gly Arg Lys Ser Phe Pro Ser Gly His Ser  
 100 105 110  
 Ser Phe Ala Phe Ala Gly Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly  
 115 120 125  
 Lys Leu His Cys Phe Thr Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe  
 130 135 140  
 Cys Ala Phe Leu Ser Pro Leu Leu Phe Ala Ala Val Ile Ala Leu Ser  
 145 150 155 160  
 Arg Thr Cys Asp Tyr Lys His His Trp Gln Asp Leu Leu Lys Cys Thr  
 165 170 175  
 Asn Thr Ala Lys  
 180

<210> 400  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 400  
 Met Cys Thr Ala Leu Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu  
 1 5 10 15  
 Lys Leu Val Asn Val Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu  
 20 25 30  
 Met Thr Phe Val Ala Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu  
 35 40 45  
 Asp Ser Pro Ala Asn Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu  
 50 55 60  
 Pro Glu Gly Cys Ser Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp  
 65 70 75 80  
 Pro Pro Glu Val Pro Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser  
 85 90 95  
 Thr Ser Ser Leu Thr Asp Thr Asp Val Gln Val Ser Pro Met Leu Val  
 100 105 110  
 Ala Gly Val Asn His Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr



130                      135                      140  
 Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His  
 145                      150                      155                      160  
 Tyr Ile Arg His Ala Arg Gly Glu Leu  
                          165

<210> 403  
 <211> 367  
 <212> PRT  
 <213> Homo sapiens

<400> 403  
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro  
 1                      5                      10                      15  
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp  
                          20                      25                      30  
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val  
                          35                      40                      45  
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val  
                          50                      55                      60  
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro  
 65                      70                      75                      80  
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu  
                          85                      90                      95  
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp  
                          100                      105                      110  
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val  
                          115                      120                      125  
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln  
                          130                      135                      140  
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly  
 145                      150                      155                      160  
 Cys Ile Leu His Leu Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr  
                          165                      170                      175  
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu  
                          180                      185                      190  
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu  
                          195                      200                      205  
 Ser Lys Gln Lys Lys Leu Met Ala Lys Ile Leu Glu His Asp Asp Val  
                          210                      215                      220  
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln  
 225                      230                      235                      240  
 Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys  
                          245                      250                      255  
 Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu  
                          260                      265                      270  
 Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys  
                          275                      280                      285  
 Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg  
                          290                      295                      300  
 Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr  
 305                      310                      315                      320  
 Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg  
                          325                      330                      335  
 Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly  
                          340                      345                      350  
 Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Tyr Ile  
                          355                      360                      365

<210> 404  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 404  
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser  
 1 5 10 15  
 Pro Val Pro Val  
 20

<210> 405  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 405  
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val  
 1 5 10 15  
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val  
 20 25 30  
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu  
 35 40 45  
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys  
 50 55 60  
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala  
 65 70 75 80  
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met  
 85 90 95  
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu  
 100 105 110  
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile  
 115 120 125  
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile  
 130 135 140  
 Ile Arg Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu  
 145 150 155 160  
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile  
 165 170 175  
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser  
 180 185 190  
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser  
 195 200 205  
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr  
 210 215 220  
 Val  
 225

<210> 406  
 <211> 378  
 <212> PRT  
 <213> Homo sapiens

<400> 406  
 Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu Tyr Gln  
 1 5 10 15  
 Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu Glu Trp



<210> 408  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<400> 408

Met	Ala	Trp	Arg	Gly	Trp	Ala	Gln	Arg	Gly	Trp	Gly	Cys	Gly	Gln	Ala
1				5					10					15	
Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	Leu	Thr	Ala	Val
			20					25					30		
Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	Phe	Phe	Ile	Gln
		35					40					45			
Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	Glu	Pro	Arg	Arg
	50					55				60					
Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	Ser	Ala	Leu	Ile
65					70					75					80
Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	Tyr	Pro	Ile	Arg
				85					90					95	
Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	Thr	Gly	Cys	Ala
			100						105					110	
Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	Lys	Ser	Arg	Val
		115					120					125			
Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	Asp	Ser	Ile	Arg
	130					135					140				
Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	Lys	Trp	Trp	Asn
145					150					155					160
Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	Ile	Ala	Ala	Asn
			165						170					175	
Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	Gln	Arg	Thr	Met
			180					185					190		
Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	Leu	Cys	Ser	Pro
		195				200						205			
Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	His	Met	Ala	Ala
	210					215					220				
Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	Val	Asn	Ile	Leu
225				230					235					240	
Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	Gly	Val	Ile	Ser
			245						250					255	
Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	Arg	Tyr	Gly	Pro
		260					265						270		
Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	Asp	Thr	Ala	Gly
		275					280					285			
Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	His	Leu	Gly	Gly
	290					295					300				
Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His	Glu	Leu	Ile	Trp
305				310						315				320	
Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu	Ile	Arg	Thr	Asn
			325						330					335	
Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys							
			340					345							

<210> 409  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens

<400> 409

Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser Ser Val  
 1 5 10 15  
 Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe Arg Gln  
 20 25 30  
 Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu  
 35 40 45  
 Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu  
 50 55 60  
 Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser  
 65 70 75 80  
 Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Ile Thr  
 85 90 95  
 Ile Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met  
 100 105 110  
 Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser  
 115 120 125  
 Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser  
 130 135 140  
 Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly  
 145 150 155 160  
 Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp  
 165 170 175  
 Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile  
 180 185 190  
 Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu  
 195 200 205  
 Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile  
 210 215 220  
 Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser  
 225 230 235

<210> 410  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
 Met Asn Thr Glu Ala Glu Gln Gln Leu Leu His His Ala Arg Asn Gly  
 1 5 10 15  
 Asn Ala Glu Glu Val Arg Gln Leu Leu Glu Thr Met Ala Ser Asn Glu  
 20 25 30  
 Val Ile Ala Asp Ile Asn Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly  
 35 40 45  
 Trp Thr Pro Leu His Leu Ala Cys Tyr Phe Gly His Arg Gln Val Val  
 50 55 60  
 Gln Asp Leu Leu Lys Ala Gly Ala Glu Val Asn Val Leu Asn Asp Met  
 65 70 75 80  
 Gly Asp Thr Pro Leu His Arg Ala Ala Phe Thr Gly Arg Lys Val Lys  
 85 90 95  
 Ile Ile Leu Cys Ser Met Phe Val Ser Glu Val Phe Gly Gly Val Val  
 100 105 110  
 Thr Ile Val Phe Ser Val Ile Thr Ile  
 115 120

<210> 411  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 411

Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro  
1 5 10 15  
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu  
20 25 30  
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu  
35 40 45  
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val  
50 55 60  
Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu  
65 70 75 80  
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu  
85 90 95  
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu  
100 105 110  
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn  
115 120 125  
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val  
130 135 140  
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val  
145 150 155 160  
His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
165 170

<210> 412

<211> 236

<212> PRT

<213> Homo sapiens

<400> 412

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Lys  
1 5 10 15  
Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala  
20 25 30  
Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu  
35 40 45  
Ser Val Leu Lys Leu His His Ser Leu Gln Gln Ser Glu Pro Asp Leu  
50 55 60  
Arg His Leu Val Leu Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser  
65 70 75 80  
Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala  
85 90 95  
Pro Ser Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser  
100 105 110  
Ala Ser Met Ala Ser Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu  
115 120 125  
Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser  
130 135 140  
Ile Gly Gly Ala Ala Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro  
145 150 155 160  
Ala Thr Gly Cys Leu Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp  
165 170 175  
Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu  
180 185 190  
Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro  
195 200 205  
Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly

210	215	220
Thr Gln Ala Leu Glu Arg	Pro Pro Gly Pro Gly Arg	
225	230	235

<210> 413  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<400> 413

Met	Lys	Gly	Leu	Tyr	Phe	Gln	Gln	Ser	Ser	Thr	Asp	Glu	Glu	Ile	Thr
1			5						10					15	
Phe	Val	Phe	Gln	Glu	Lys	Glu	Asp	Leu	Pro	Val	Thr	Glu	Asp	Asn	Phe
			20					25					30		
Val	Lys	Leu	Gln	Val	Lys	Ala	Cys	Ala	Leu	Ser	Gln	Ile	Asn	Thr	Lys
			35				40					45			
Leu	Leu	Ala	Glu	Met	Lys	Met	Lys	Lys	Asp	Leu	Phe	Pro	Val	Gly	Arg
			50			55					60				
Glu	Ile	Ala	Gly	Ile	Val	Leu	Asp	Val	Gly	Ser	Lys	Val	Ser	Phe	Phe
65				70						75				80	
Gln	Pro	Asp	Asp	Glu	Val	Val	Gly	Ile	Leu	Pro	Leu	Asp	Ser	Glu	Asp
			85						90					95	
Pro	Gly	Leu	Cys	Glu	Val	Val	Arg	Val	His	Glu	His	Tyr	Leu	Val	His
			100					105					110		
Lys	Pro	Glu	Lys	Val	Thr	Trp	Thr	Glu	Ala	Ala	Gly	Ser	Ile	Arg	Asp
			115				120					125			
Gly	Val	Arg	Ala	Tyr	Thr	Ala	Leu	His	Tyr	Leu	Ser	His	Leu	Ser	Pro
			130			135					140				
Gly	Lys	Ser	Val	Leu	Ile	Met	Asp	Gly	Ala	Ser	Ala	Phe	Gly	Thr	Ile
145				150						155				160	
Ala	Ile	Gln	Leu	Ala	His	His	Arg	Gly	Ala	Lys	Val	Phe	Gln	Gln	His
			165					170					175		
Ala	Ala	Leu	Lys	Ile	Ser	Ser	Ala	Leu	Lys	Asp	Ser	Asp	Leu	Pro	
			180					185					190		

<210> 414  
 <211> 389  
 <212> PRT  
 <213> Homo sapiens

<400> 414

Met	Ala	Glu	Pro	Asp	Pro	Ser	His	Pro	Leu	Glu	Thr	Gln	Ala	Gly	Lys
1			5						10					15	
Val	Gln	Glu	Ala	Gln	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Gly	Gly	Ala	Ala
			20					25					30		
Gly	Gly	Glu	Ala	Asp	Met	Asp	Phe	Leu	Arg	Asn	Leu	Phe	Ser	Gln	Thr
		35				40					45				
Leu	Ser	Leu	Gly	Ser	Gln	Lys	Glu	Arg	Leu	Leu	Asp	Glu	Leu	Thr	Leu
		50				55					60				
Glu	Gly	Val	Ala	Arg	Tyr	Met	Gln	Ser	Glu	Arg	Cys	Arg	Arg	Val	Ile
65				70					75					80	
Cys	Leu	Val	Gly	Ala	Gly	Ile	Ser	Thr	Ser	Ala	Gly	Ile	Pro	Asp	Phe
			85					90					95		
Arg	Ser	Pro	Ser	Thr	Gly	Leu	Tyr	Asp	Asn	Leu	Glu	Lys	Tyr	His	Leu
			100					105					110		
Pro	Tyr	Pro	Glu	Ala	Ile	Phe	Glu	Ile	Ser	Tyr	Phe	Lys	Lys	His	Pro
			115				120					125			
Glu	Pro	Phe	Phe	Ala	Leu	Ala	Lys	Glu	Leu	Tyr	Pro	Gly	Gln	Phe	Lys

130 135 140  
 Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu  
 145 150 155 160  
 Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala  
 165 170 175  
 Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr  
 180 185 190  
 Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp  
 195 200 205  
 Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys  
 210 215 220  
 Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro  
 225 230 235 240  
 Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu  
 245 250 255  
 Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu  
 260 265 270  
 Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu  
 275 280 285  
 Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly  
 290 295 300  
 Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp  
 305 310 315 320  
 Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly  
 325 330 335  
 Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile  
 340 345 350  
 Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser  
 355 360 365  
 Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu  
 370 375 380  
 Arg Glu Lys Pro Gln  
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<210> 415  
 <211> 481  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp  
 1 5 10 15  
 Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln  
 20 25 30  
 Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu  
 35 40 45  
 Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp  
 50 55 60  
 Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln  
 65 70 75 80  
 Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys  
 85 90 95  
 Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala  
 100 105 110  
 Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg  
 115 120 125  
 Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu  
 130 135 140

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Lys Gly Asp His Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu  
 145 150 155 160  
 Pro Lys Ser Lys Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val  
 165 170 175  
 Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys  
 180 185 190  
 Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu  
 195 200 205  
 Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile  
 210 215 220  
 Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln  
 225 230 235 240  
 Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr  
 245 250 255  
 Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys  
 260 265 270  
 Val Leu Asp Leu Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser  
 275 280 285  
 Glu Glu Lys Ala Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser  
 290 295 300  
 Ala Val Ile Gly Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly  
 305 310 315 320  
 Ser Gly Gln Leu Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser  
 325 330 335  
 Val Gln Gly Phe Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg  
 340 345 350  
 Tyr Leu Arg Arg Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu  
 355 360 365  
 Leu Lys Ala Val Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser  
 370 375 380  
 Ser Leu Leu Val Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu  
 385 390 395 400  
 Asp Ser Asp Ala Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp  
 405 410 415  
 Glu Ser Ala Gly Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val  
 420 425 430  
 Asp Val Arg Met Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly  
 435 440 445  
 Glu Asp Thr Val Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly  
 450 455 460  
 Leu Gln Ser Leu Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly  
 465 470 475 480  
 Glu

<210> 416  
 <211> 354  
 <212> PRT  
 <213> Homo sapiens

<400> 416  
 Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro  
 1 5 10 15  
 Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His  
 20 25 30  
 Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr  
 35 40 45  
 Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro  
 50 55 60

Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln  
 65 70 75 80  
 Val Leu Val Val Gly Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala  
 85 90 95  
 Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr  
 100 105 110  
 Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met  
 115 120 125  
 Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln  
 130 135 140  
 Val Arg Val Tyr Glu Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser  
 145 150 155 160  
 Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys  
 165 170 175  
 Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe  
 180 185 190  
 Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu  
 195 200 205  
 Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val  
 210 215 220  
 Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser  
 225 230 235 240  
 Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly  
 245 250 255  
 Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala  
 260 265 270  
 Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly  
 275 280 285  
 Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu  
 290 295 300  
 Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys  
 305 310 315 320  
 Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly  
 325 330 335  
 Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp  
 340 345 350  
 Gly Val

<210> 417  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 417  
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr  
 1 5 10 15  
 Phe Val Phe Gln  
 20

<210> 418  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 418  
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr  
 1 5 10 15  
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe



Cys	Ala	Ala	Leu	Trp	Trp	His	Lys	Lys	Gly	Leu	Ala	Val	Leu	Phe	Cys
		115					120					125			
Ile	Leu	Gln	Phe	Leu	Ser	Met	Thr	Trp	Tyr	Ser	Leu	Ser	Tyr	Ile	Pro
	130					135					140				
Tyr	Ala	Arg	Asp	Ala	Val	Ile	Lys	Cys	Cys	Ser	Ser	Leu	Leu	Ser	
145					150						155				

<210> 420  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 420															
Met	Glu	Gln	Arg	Leu	Ala	Glu	Phe	Arg	Ala	Ala	Arg	Lys	Arg	Ala	Gly
1				5					10					15	
Leu	Ala	Ala	Gln	Pro	Pro	Ala	Ala	Ser	Gln	Gly	Ala	Gln	Thr	Pro	Gly
			20					25					30		
Glu	Lys	Ala	Glu	Ala	Ala	Ala	Thr	Leu	Lys	Ala	Ala	Pro	Gly	Trp	Leu
		35					40					45			
Lys	Arg	Phe	Leu	Val	Trp	Lys	Pro	Arg	Pro	Ala	Ser	Ala	Arg	Ala	Gln
	50					55					60				
Pro	Gly	Leu	Val	Gln	Glu	Ala	Ala	Gln	Pro	Gln	Gly	Ser	Thr	Ser	Glu
65				70						75					80
Thr	Pro	Trp	Asn	Thr	Ala	Ile	Pro	Leu	Pro	Ser	Cys	Trp	Asp	Gln	Ser
				85					90					95	
Phe	Leu	Thr	Asn	Ile	Thr	Phe	Leu	Lys	Val	Leu	Leu	Trp	Leu	Val	Leu
			100					105					110		
Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu	Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu
		115					120					125			
Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val	Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys
	130					135					140				
Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr	Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu
145					150					155					160
Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala	Glu	Gln	Leu	Glu	Arg	Glu	Leu	Gln
				165				170						175	
Leu	Arg	Pro	Leu	Ala	Gly	Arg									
			180												

<210> 421  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 421															
Met	Ala	Ala	Pro	Arg	Arg	Gly	Arg	Gly	Ser	Ser	Thr	Val	Leu	Ser	Ser
1				5					10					15	
Val	Pro	Leu	Gln	Met	Leu	Phe	Tyr	Leu	Ser	Gly	Thr	Tyr	Tyr	Ala	Leu
			20					25					30		
Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Met	Ile	Thr	Tyr	Lys	Ser	Gln	Val	Phe
		35					40					45			
Ser	Tyr	Pro	His	Arg	Tyr	Leu	Val	Leu	Asp	Leu	Ala	Leu	Leu	Phe	Leu
	50					55					60				
Met	Gly	Ile	Leu	Glu	Ala	Val	Arg	Leu	Tyr	Leu	Gly	Thr	Arg	Gly	Asn
65				70						75					80
Leu	Thr	Glu	Ala	Glu	Arg	Pro	Leu	Ala	Ala	Ser	Leu	Ala	Leu	Thr	Ala
				85					90					95	
Gly	Thr	Ala	Leu	Leu	Ser	Ala	His	Phe	Leu	Leu	Trp	Gln	Ala	Leu	Val
			100					105					110		

Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly  
115 120 125  
Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg  
130 135 140

<210> 422  
<211> 73  
<212> PRT  
<213> Homo sapiens

<400> 422  
Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu  
1 5 10 15  
Pro Val Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val  
20 25 30  
Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala  
35 40 45  
Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu  
50 55 60  
His Lys Phe His Gly Gln Val Gln Phe  
65 70

<210> 423  
<211> 142  
<212> PRT  
<213> Homo sapiens

<400> 423  
Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser  
1 5 10 15  
Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn  
20 25 30  
Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His  
35 40 45  
His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser  
50 55 60  
Ser Leu Leu Cys Arg Pro Leu Gln Leu Ser Phe Leu Val Ile Gln Ser  
65 70 75 80  
Val Arg Met Arg Ala Cys Gly Cys Asp Ser Gly His Cys Arg Ile Leu  
85 90 95  
Gly Arg Tyr Ser Leu Leu Gly Trp Ser Gln Gly His Arg Ala Arg Gly  
100 105 110  
Arg Gly Gly Val Ser Leu Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser  
115 120 125  
Glu Gly Gln Gly Gln Trp Leu Met Pro Val Ile Pro Ala Phe  
130 135 140

<210> 424  
<211> 149  
<212> PRT  
<213> Homo sapiens

<400> 424  
Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr Ala  
1 5 10 15  
Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro  
20 25 30  
Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala

35 40 45  
 Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala Asp  
 50 55 60  
 Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys Pro  
 65 70 75 80  
 Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser Leu  
 85 90 95  
 Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro Glu  
 100 105 110  
 Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val Gln  
 115 120 125  
 Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser Arg  
 130 135 140  
 Asn Asp Glu Thr Leu  
 145

<210> 425  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<400> 425  
 Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys Asn Phe Ala Leu Ser  
 1 5 10 15  
 Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu Val Glu Lys His Asn  
 20 25 30  
 Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly Pro Ser Leu Ser Ser  
 35 40 45  
 Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu Ile Leu Val Ala Thr  
 50 55 60  
 Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His  
 65 70 75

<210> 426  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 426  
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn  
 1 5 10 15  
 Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser  
 20 25 30  
 Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln  
 35 40 45  
 Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser  
 50 55 60  
 Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp  
 65 70 75 80  
 Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu  
 85 90 95  
 Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu  
 100 105 110  
 Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe  
 115 120 125  
 Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu  
 130 135 140  
 Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile

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Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala Pro  
 20 25 30  
 Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu Cys  
 35 40 45  
 Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser His  
 50 55 60  
 Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr Asp  
 65 70 75 80  
 Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp  
 85 90 95

<210> 430  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 430  
 Met Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu  
 1 5 10 15  
 Pro Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His  
 20 25 30  
 Cys Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu  
 35 40 45  
 Leu Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val  
 50 55 60  
 Val Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn  
 65 70 75 80  
 Ala Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu  
 85 90 95  
 Leu Ser Leu

<210> 431  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 431  
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu  
 1 5 10 15  
 Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln  
 20 25 30  
 Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala  
 35 40 45  
 Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val Cys  
 50 55 60  
 Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile  
 65 70 75 80  
 Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val Met  
 85 90 95  
 Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu  
 100 105 110  
 Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys  
 115 120

<210> 432  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

<400> 432

Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser  
1 5 10 15  
Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys  
20 25 30  
Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr  
35 40 45  
Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln  
50 55 60  
Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp  
65 70 75 80  
Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile  
85 90 95  
Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln  
100 105 110  
Glu Arg Thr Ser Ser Leu  
115

<210> 433

<211> 49

<212> PRT

<213> Homo sapiens

<400> 433

Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro  
1 5 10 15  
Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe  
20 25 30  
Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln  
35 40 45  
His

<210> 434

<211> 89

<212> PRT

<213> Homo sapiens

<400> 434

Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val  
1 5 10 15  
Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp  
20 25 30  
Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu  
35 40 45  
Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly  
50 55 60  
Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val Trp His  
65 70 75 80  
Glu Asn Ser Gln Glu Glu Arg Lys Tyr  
85

<210> 435

<211> 87

<212> PRT

<213> Homo sapiens

<400> 435

Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys Ser  
 1 5 10 15  
 Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val Phe  
 20 25 30  
 Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val Glu  
 35 40 45  
 Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu Val  
 50 55 60  
 Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly Asp  
 65 70 75 80  
 Leu Leu Pro Val Asn Arg Ile  
 85

<210> 436  
 <211> 45  
 <212> PRT  
 <213> Homo sapiens

<400> 436  
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu  
 1 5 10 15  
 Asp Gly Pro Gln Ser Gln Thr Pro Glu Asp Cys Pro Ala Arg Pro Glu  
 20 25 30  
 His Gln Gln Asp Gly Arg Gly His Leu Pro Lys His Glu  
 35 40 45

<210> 437  
 <211> 65  
 <212> PRT  
 <213> Homo sapiens

<400> 437  
 Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile His Ser His  
 1 5 10 15  
 Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln Trp Leu Pro  
 20 25 30  
 Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys Ser Cys Arg  
 35 40 45  
 Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Phe Ser Phe Leu Ile  
 50 55 60  
 Ser  
 65

<210> 438  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 438  
 Met Arg Lys Lys Cys Lys Cys Phe Thr Ile Lys Lys Thr Asn Thr Tyr  
 1 5 10 15  
 Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln Lys Glu Ala Ile Ser Ile  
 20 25 30  
 Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro Leu Trp Val Thr Arg Leu  
 35 40 45  
 Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu  
 50 55 60  
 Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser

65				70				75				80			
Ser	Arg	Asn	Leu	Arg	Tyr	Phe	Ile	Val	Cys	Arg	Asp	Ala	Ser	Ser	Tyr
				85					90					95	
Thr	Pro	Gln	Ser	Leu	Ile	Ser	Gly	Tyr	Ile	Gly	Pro	Cys	Gln	His	Gln
				100				105					110		

<210> 439  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 439															
Met	Val	Phe	Gly	Ala	Met	Val	Leu	Leu	Val	Gly	Leu	Glu	Glu	Leu	Thr
1				5					10					15	
Asn	Ile	Arg	Asn	Val	Glu	Arg	Leu	Lys	Lys	Asp	Leu	Arg	Ala	Ser	Tyr
			20					25					30		
Cys	Leu	Ile	Asp	Ser	Phe	Leu	Gly	Asp	Ser	Glu	Leu	Ile	Gly	Asp	Leu
		35					40					45			
Thr	Gln	Cys	Val	Asp	Cys	Val	Ile	Pro	Pro	Glu	Gly	Ser	Leu	Leu	Gln
	50					55				60					
Ile	Ser	Ser	Tyr	Leu	Tyr	Leu	Asn	Thr	Ala	Leu	Val	Asp	Leu	Pro	Gly
65				70					75					80	
Val	Ala	Ala	Ser	Gln	Ala	Cys	Asp	Ser	Gln	Gln	Val	Thr	Trp	Leu	Leu
			85					90					95		
Tyr	Val	Ala	Asn	Gly	Ala	Tyr	Ser	Ala	Cys	Asn	Arg	Pro	Gly		
			100					105					110		

<210> 440  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 440															
Thr	Ser	Ser	Ser	Gly	Ala	Glu	Val	Thr	Met	Ala	Ala	Ala	Leu	Ala	Arg
1				5				10						15	
Leu	Gly	Leu	Arg	Pro	Val	Lys	Gln	Val	Arg	Val	Gln	Phe	Cys	Pro	Phe
			20					25					30		
Glu	Lys	Asn	Val	Glu	Ser	Thr	Arg	Thr	Phe	Leu	Gln	Thr	Val	Ser	Ser
		35				40						45			
Glu	Lys	Val	Arg	Ser	Thr	Asn	Leu	Asn	Cys	Ser	Val	Ile	Ala	Asp	Val
	50					55				60					
Arg	His	Asp	Gly	Ser	Glu	Pro	Cys	Val	Asp	Val	Leu	Phe	Gly	Asp	Gly
65				70					75					80	
His	Arg	Leu	Ile	Met	Arg	Gly	Ala	His	Leu	Thr	Ala	Leu	Glu	Met	Leu
			85					90					95		
Thr	Ala	Phe	Ala	Ser	His	Ile	Arg	Ala	Arg	Asp	Ala	Ala	Gly	Ser	Gly
			100					105					110		
Asp	Lys	Pro	Gly	Ala	Asp	Thr	Gly	Arg							
		115					120								

<210> 441  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 441															
Met	Leu	Ala	Arg	Ala	Thr	Phe	Arg	Ala	Ala	Ser	Ala	Pro	Thr	Leu	Val
1				5					10					15	

Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr  
 20 25 30  
 His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys  
 35 40 45  
 Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala  
 50 55 60  
 Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala  
 65 70 75 80  
 Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala  
 85 90 95  
 Phe Val Asp

<210> 442  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 442  
 Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala  
 1 5 10 15  
 Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe  
 20 25 30  
 Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu  
 35 40 45  
 Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys  
 50 55 60  
 His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu  
 65 70 75 80  
 Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu  
 85 90 95  
 Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu  
 100 105 110  
 Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val  
 115 120 125  
 Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp  
 130 135 140  
 Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser  
 145 150 155 160  
 Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu  
 165 170 175  
 Leu Pro Lys Lys Lys Lys Lys  
 180

<210> 443  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 443  
 Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr  
 1 5 10 15  
 Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr  
 20 25 30  
 Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys  
 35 40 45  
 Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr  
 50 55 60  
 Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu

65		70		75		80							
Gly	Ser	Glu	Glu	Leu	Phe	Ser	Ser	Val	Cys	Trp	Arg	Ser	Arg
				85					90				

<210> 444  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 444  
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu  
 1 5 10 15  
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly  
 20 25 30  
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly  
 35 40 45  
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly  
 50 55 60  
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly  
 65 70 75 80  
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe  
 85 90 95  
 Met Ala Ile Gly Met Gly Ile Arg Cys  
 100 105

<210> 445  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 445  
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu  
 1 5 10 15  
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg  
 20 25 30  
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn  
 35 40 45  
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln  
 50 55 60  
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu  
 65 70 75 80  
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Cys Lys Leu  
 85 90 95  
 Leu Cys Gln Lys Leu Met Glu Lys Thr Gly Ile Leu Leu Leu Cys Ala  
 100 105 110  
 Phe Gly Val Ser Gln Gly Pro Ala Gln Ser Gln Val Glu Val Ser Leu  
 115 120 125  
 Gly Pro Gly Thr Asp Tyr Arg Thr Leu Gly Lys Thr Leu His Cys His  
 130 135 140  
 Val Thr Gln Phe Pro His Leu Pro Asp Gly Cys Cys Cys Glu Asn Tyr  
 145 150 155 160  
 Glu Met Lys

<210> 446  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<400> 446

```
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1          5          10          15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
          20          25          30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
          35          40          45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
          50          55          60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65          70          75          80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
          85          90          95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
          100          105          110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
          115          120          125
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<210> 447

<211> 96

<212> PRT

<213> Homo sapiens

<400> 447

```
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1          5          10          15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
          20          25          30
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
          35          40          45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
          50          55          60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65          70          75          80
Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
          85          90          95
```

<210> 448

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 114

<223> Xaa = Glu,Val

<220>

<221> UNSURE

<222> 113

<223> Xaa = His,Gln

<220>

<221> UNSURE

<222> 115

<223> Xaa = Ile,Val

<400> 448

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile Thr  
 1 5 10 15  
 Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met Lys  
 20 25 30  
 Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg Leu  
 35 40 45  
 Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met Val  
 50 55 60  
 Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu Ser  
 65 70 75 80  
 Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys Thr  
 85 90 95  
 Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln Pro  
 100 105 110  
 Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser Val  
 115 120 125  
 Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys Ala  
 130 135 140  
 Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys Cys  
 145 150 155 160

<210> 449  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 449  
 Met Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp  
 1 5 10 15  
 Val Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu  
 20 25 30  
 Cys Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr  
 35 40 45  
 Trp Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu  
 50 55 60  
 Leu Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser  
 65 70 75 80  
 Val Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys  
 85 90 95  
 Lys Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu  
 100 105 110  
 Leu Gly Gly Ile Ser  
 115

<210> 450  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 450  
 Met Cys Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val  
 1 5 10 15  
 Leu Ala Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln  
 20 25 30  
 Asp Pro Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala  
 35 40 45  
 Ser Lys Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala  
 50 55 60

Gln	Gln	Ile	Gly	Ser	His	His	Ile	Ser	Leu	Asn	Ile	Asp	Pro	Ala	Val
65					70					75					80
Lys	Ala	Val	Met	Gly	Ile	Phe	Ser	Leu	Val	Thr	Gly	Lys	Ser	Pro	Leu
				85					90					95	
Phe	Ala	Ala	His	Gly	Gly	Ser	Ser	Arg	Glu	Asn	Leu	Ala	Leu	Gln	Asn
			100					105					110		
Val	Gln	Ala	Arg	Ile	Arg	Met	Val	Leu	Ala	Tyr	Leu	Phe	Ala	Gln	Leu
		115				120						125			
Ser	Leu	Trp	Ser	Arg	Gly	Val	His	Gly	Gly	Leu	Leu	Val	Leu	Gly	Ser
	130				135						140				
Ala	Asn	Val	Asp	Glu	Ser	Leu	Leu	Gly	Tyr	Leu	Thr	Lys	Tyr	Asp	Cys
145				150					155						160
Ser	Ser	Ala	Asp	Ile	Asn	Pro	Ile	Gly	Gly	Ile	Ser	Lys	Thr	Asp	Leu
			165					170						175	
Arg	Ala	Phe	Val	Gln	Phe	Cys	Ile	Gln	Arg	Phe	Gln	Leu	Pro	Ala	Leu
		180						185					190		
Gln	Ser	Ile	Leu	Leu	Ala	Pro	Ala	Thr	Ala	Glu	Leu	Glu	Pro	Leu	Ala
	195					200						205			
Asp	Gly	Gln	Val	Ser	Gln	Thr	Asp	Glu	Glu	Asp	Met	Gly	Met	Thr	Tyr
	210					215					220				
Ala	Glu	Leu	Ser	Val	Tyr	Gly	Lys	Leu	Arg	Lys	Val	Ala	Lys	Met	Gly
225				230					235						240
Pro	Tyr	Ser	Met	Phe	Cys	Lys	Leu	Leu	Gly	Met	Trp	Arg	His	Ile	Cys
			245						250					255	
Thr	Pro	Arg	Gln	Val	Ala	Asp	Lys	Val	Lys	Arg	Phe	Phe	Ser	Lys	Tyr
		260					265						270		
Ser	Met	Asn	Arg	His	Lys	Met	Thr	Thr	Leu	Thr	Pro	Ala	Tyr	His	Ala
	275					280						285			
Glu	Asn	Tyr	Ser	Pro	Glu	Asp	Asn	Arg	Phe	Asp	Leu	Arg	Pro	Phe	Leu
	290				295					300					
Tyr	Asn	Thr	Ser	Trp	Pro	Trp	Gln	Phe	Arg	Cys	Ile	Glu	Asn	Gln	Val
305				310					315						320
Leu	Gln	Leu	Glu	Arg	Ala	Glu	Pro	Gln	Ser	Leu	Asp	Gly	Val	Asp	
			325					330						335	

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys,Asn

<400> 451

Met	Cys	Trp	Val	Ile	Asn	His	Ala	Ile	Leu	Pro	Arg	Met	Arg	Met	His
1				5					10					15	
Ser	Lys	Arg	Gln	Thr	Ile	Thr	Arg	His	Ser	Ala	Ser	Leu	Ser	Phe	His
		20					25					30			
Ala	Leu	Pro	Arg	Ser	Ala	Phe	Leu	Gln	Leu	Cys	Leu	Leu	Arg	Gln	Ile
	35					40					45				
His	Gln	Ile	Pro	Cys	Leu	Ser	Ile	Phe	Ser	Ser	Thr	Leu	Arg	Ala	Gln
	50				55					60					
Thr	His	Asp	Ser	Gly	Ile	Gly	Cys	Thr	Thr	Ala	Xaa	Pro	Gly	Gly	Arg
65				70					75						80
Arg	Gln	Glu	Gln	Leu	Arg										
			85												

<210> 452  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 452  
 Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys  
 1 5 10 15  
 Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg  
 20 25 30  
 Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro  
 35 40 45  
 Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu  
 50 55 60  
 His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys  
 65 70 75 80  
 Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala  
 85 90

<210> 453  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 453  
 Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe  
 1 5 10 15  
 Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu  
 20 25 30  
 Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val  
 35 40 45  
 Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val  
 50 55 60  
 Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln  
 65 70 75 80  
 Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln  
 85 90 95  
 Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn  
 100 105

<210> 454  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 454  
 Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg  
 1 5 10 15  
 Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe  
 20 25 30  
 Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys  
 35 40 45  
 Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr  
 50 55 60  
 Glu Leu Ser Pro Ser Glu Tyr Lys Ala Met Val Leu Ala Gly Leu  
 65 70 75 80  
 Arg Pro Glu Ile Val Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp

				85					90					95			
Thr	Tyr	Gln	Val	His	Gln	Glu	Arg	Leu	Tyr	Gln	Glu	Tyr	Asn	Phe	Ser		
			100					105					110				
Lys	Ala	Glu	Gly	His	Leu	Lys	Gln	Met	Glu	Lys	Ile	Tyr	Thr	Gln	Gln		
		115					120					125					
Ile	Gln	Ser	Lys	Asp	Val	Glu	Leu	Thr	Ser	Met	Lys	Gly	Glu	Val	Thr		
	130					135					140						
Ser	Met	Lys	Lys	Val	Leu	Glu	Glu	Tyr	Lys	Lys	Lys	Phe	Ser	Asp	Ile		
145				150					155					160			
Ser	Glu	Lys	Leu	Met	Glu	Arg	Asn	Arg	Gln	Tyr	Gln	Lys	Leu	Gln	Gly		
			165					170						175			
Leu	Tyr	Asp	Ser	Leu	Arg	Leu	Arg	Asn	Ile	Thr	Ile	Ala	Asn	His	Glu		
		180						185					190				
Gly	Thr	Leu	Glu	Pro	Ser	Met	Ile	Ala	Gln	Ser	Gly	Val	Leu	Gly	Phe		
	195					200					205						
Pro	Leu	Gly	Asn	Asn	Ser	Lys	Phe	Pro	Leu	Asp	Asn	Thr	Pro	Val	Arg		
	210					215				220							
Asn	Arg	Gly	Asp	Gly	Asp	Gly	Asp	Phe	Gln	Phe	Arg	Pro	Phe	Phe	Ala		
225				230				235						240			
Gly	Ser	Pro	Thr	Ala	Pro	Glu	Pro	Ser	Asn	Ser	Phe	Phe	Ser	Phe	Val		
			245					250						255			
Ser	Pro	Ser	Arg	Glu	Leu	Glu	Gln	Gln	Gln	Val	Ser	Ser	Arg	Ala	Phe		
		260				265							270				
Lys	Val	Lys	Arg	Ile													
		275															

<210> 455  
 <211> 173  
 <212> PRT  
 <213> Homo sapiens

Met	Leu	Val	Met	Tyr	Leu	Leu	Ala	Ala	Leu	Phe	Gly	Tyr	Leu	Thr	Phe		
1			5						10				15				
Tyr	Gly	Glu	Val	Glu	Asp	Glu	Leu	Leu	His	Ala	Tyr	Ser	Lys	Val	Tyr		
		20					25					30					
Thr	Leu	Asp	Ile	Pro	Leu	Leu	Met	Val	Arg	Leu	Ala	Val	Leu	Val	Ala		
	35					40					45						
Val	Thr	Leu	Thr	Val	Pro	Ile	Val	Leu	Phe	Pro	Ile	Arg	Thr	Ser	Val		
	50					55				60							
Ile	Thr	Leu	Leu	Phe	Pro	Lys	Arg	Pro	Phe	Ser	Trp	Ile	Arg	His	Phe		
65				70					75					80			
Leu	Ile	Ala	Ala	Val	Leu	Ile	Ala	Leu	Asn	Asn	Val	Leu	Val	Ile	Leu		
			85					90				95					
Val	Pro	Thr	Ile	Lys	Tyr	Ile	Phe	Gly	Phe	Ile	Gly	Ala	Ser	Ser	Ala		
		100					105				110						
Thr	Met	Leu	Ile	Phe	Ile	Leu	Pro	Ala	Val	Phe	Tyr	Leu	Lys	Leu	Val		
	115					120					125						
Lys	Lys	Glu	Thr	Phe	Arg	Ser	Pro	Gln	Lys	Val	Gly	Ala	Leu	Ile	Phe		
	130					135				140							
Leu	Val	Val	Gly	Ile	Phe	Phe	Met	Ile	Gly	Ser	Met	Ala	Leu	Ile	Ile		
145				150					155					160			
Ile	Asp	Trp	Ile	Tyr	Asp	Pro	Pro	Asn	Ser	Lys	His	His					
			165					170									

<210> 456  
 <211> 370  
 <212> PRT

<213> Homo sapiens

<400> 456

```
Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
1      5      10      15
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
20      25      30
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
35      40      45
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
50      55      60
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
65      70      75      80
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
85      90      95
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
100     105     110
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
115     120     125
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
130     135     140
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
145     150     155     160
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
165     170     175
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
180     185     190
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
195     200     205
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
210     215     220
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
225     230     235     240
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
245     250     255
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
260     265     270
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
275     280     285
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
290     295     300
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
305     310     315     320
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
325     330     335
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
340     345     350
Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
355     360     365
Val Glu
370
```

<210> 457

<211> 393

<212> PRT

<213> Homo sapiens

<400> 457

```

Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu
1      5      10      15
Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly
20      25      30
Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr
35      40      45
Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr
50      55      60
Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu His
65      70      75      80
Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser
85      90      95
Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr
100     105     110
Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala
115     120     125
Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn
130     135     140
Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys
145     150     155     160
Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu
165     170     175
Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His
180     185     190
Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp
195     200     205
Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr
210     215     220
Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr
225     230     235     240
Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val
245     250     255
Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg
260     265     270
Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp
275     280     285
Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn Cys
290     295     300
Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu Ser
305     310     315     320
Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu Leu
325     330     335
Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg His
340     345     350
Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala Leu
355     360     365
Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu Pro
370     375     380
Met Glu Ser Gly Lys Glu Lys Ala Thr
385     390

```

<210> 458

<211> 116

<212> PRT

<213> Homo sapiens

<400> 458

Met Val Gly Gly Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly

1                    5                    10                    15  
 Val Arg Gln Ala Asp Phe Ala Glu Gln Phe Arg Ser Tyr Ser Glu  
                   20                    25                    30  
 Ser Glu Lys Gln Trp Lys Ala Arg Met Glu Phe Ile Leu Arg His Leu  
                   35                    40                    45  
 Pro Asp Tyr Arg Asp Pro Pro Asp Gly Ser Gly Arg Leu Asp Gln Leu  
                   50                    55                    60  
 Leu Ser Leu Ser Met Val Trp Ala Asn His Leu Phe Leu Gly Cys Ser  
 65                    70                    75                    80  
 Tyr Asn Lys Asp Leu Leu Asp Lys Val Met Glu Met Ala Asp Gly Ile  
                   85                    90                    95  
 Glu Val Glu Asp Leu Pro Gln Phe Thr Thr Arg Ser Glu Leu Met Lys  
                   100                    105                    110  
 Lys His Gln Ser  
                   115

<210> 459  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 459  
 Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser  
 1                    5                    10                    15  
 Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp  
                   20                    25                    30  
 Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu  
                   35                    40                    45  
 Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala  
                   50                    55                    60  
 Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly  
 65                    70                    75                    80  
 Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln Thr Glu Asp Ser Trp  
                   85                    90                    95  
 Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro Leu Thr Val Arg Arg  
                   100                    105                    110  
 His Val Pro Ala Val Trp Val Leu Ser Arg Asp Pro Leu Asp Pro  
                   115                    120                    125  
 Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser  
                   130                    135                    140  
 Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg Arg Arg Ala Arg Asp  
 145                    150                    155                    160  
 Thr Arg Ser

<210> 460  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 460  
 Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly  
 1                    5                    10                    15  
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala  
                   20                    25                    30  
 Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu  
                   35                    40                    45  
 Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu  
                   50                    55                    60

Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr  
 65 70 75 80  
 Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys  
 85 90 95  
 Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr  
 100 105 110  
 Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp  
 115 120 125  
 Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser  
 130 135 140  
 Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala  
 145 150 155 160  
 Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu  
 165 170 175  
 Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr  
 180 185 190  
 Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly  
 195 200 205  
 Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu  
 210 215 220  
 Lys Thr Ile His Glu Glu  
 225 230

<210> 461  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> 95  
 <223> Xaa = Cys, Trp

<400> 461  
 Met Glu Arg Pro Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu  
 1 5 10 15  
 Phe Arg Asn Glu Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe  
 20 25 30  
 Phe Thr Ala Leu Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr  
 35 40 45  
 Lys Ser Tyr Ile Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser  
 50 55 60  
 Tyr Phe Tyr Ala Ala Ile Val Ala Val Val Ala Val His Val Val Leu  
 65 70 75 80  
 Ala Leu Phe Val Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg  
 85 90 95  
 Glu Gly Lys Gln Asp  
 100

<210> 462  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 462  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala  
 1 5 10 15  
 Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu

20 25 30  
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg  
 35 40 45  
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu  
 50 55 60  
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp  
 65 70 75 80  
 Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro  
 85 90

<210> 463  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 463  
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala  
 1 5 10 15  
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu  
 20 25 30  
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Lys Leu Leu Pro Leu Asp  
 35 40 45  
 Thr Tyr Val Glu Ser Pro Ala Ala Val Met Glu Leu Val Pro Ser Asp  
 50 55 60  
 Lys Glu Arg Gly Leu Gln Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile  
 65 70 75 80  
 Leu Arg Arg Ala Gly Cys Val Arg Ala Leu Ala Lys Ile Glu Arg Phe  
 85 90 95  
 Glu Phe Tyr Glu Arg Ala Lys Lys Ala Phe Ala Val Val Ala Thr Gly  
 100 105 110  
 Glu Thr Ala Leu Tyr Gly Asn Leu Ile Leu Arg Lys Gly Val Leu Ala  
 115 120 125  
 Leu Asn Pro Leu Leu  
 130

<210> 464  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala  
 1 5 10 15  
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu  
 20 25 30  
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Ala Ala Ala Pro Gly His  
 35 40 45  
 Leu Cys Gly Glu Ser Gly Cys Ser His Gly Ala Gly Ala Gln Arg Gln  
 50 55 60  
 Gly Glu Gly Pro Ala Asp Pro Ser Val Asp Gly Val Arg Val His Pro  
 65 70 75 80  
 Thr Gln Gly Arg Leu Cys Glu Ser Pro Gly Lys Asp Arg Glu Val  
 85 90 95

<210> 465  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 465

Met Thr Pro Ile Lys Leu Leu Asn Leu Thr Ser Arg Tyr Asn Phe Arg  
1 5 10 15  
Arg Thr Phe Gly Ile Glu Leu Ser Ser Asn Ser Ser Tyr Cys Lys Arg  
20 25 30  
Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys Glu Cys Glu Cys Asn Trp  
35 40 45  
Leu His Leu Glu Ser Asp Thr Leu Lys Lys Leu Pro Ile Ile Ser Pro  
50 55 60  
Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu Tyr Phe Ser Gly Gln Leu  
65 70 75 80  
Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu Ile Lys Leu  
85 90

<210> 466

<211> 500

<212> PRT

<213> Homo sapiens

<400> 466

Met Glu Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr  
1 5 10 15  
Val Glu Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile  
20 25 30  
Gln Asp Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe  
35 40 45  
Arg Asp Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys  
50 55 60  
Ile Gln Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu  
65 70 75 80  
Cys Lys Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu  
85 90 95  
Asp Lys Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His  
100 105 110  
Pro Gln Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro  
115 120 125  
Asp Gly Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val  
130 135 140  
Gly Gln Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe  
145 150 155 160  
Met Glu Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys  
165 170 175  
Glu Leu Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His  
180 185 190  
Lys Glu Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu  
195 200 205  
Lys Leu His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu  
210 215 220  
Leu Arg Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu  
225 230 235 240  
Ser Gln Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val Ser  
245 250 255  
Ile Gln Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys Asp  
260 265 270  
Ile Thr Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala  
275 280 285  
Thr Arg Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly

290 295 300  
 Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro  
 305 310 315 320  
 Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu  
 325 330 335  
 Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys  
 340 345 350  
 Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu  
 355 360 365  
 Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val  
 370 375 380  
 Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile  
 385 390 395 400  
 Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu  
 405 410 415  
 Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe  
 420 425 430  
 Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp  
 435 440 445  
 Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His  
 450 455 460  
 Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe  
 465 470 475 480  
 Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile  
 485 490 495  
 Leu His Pro Gln  
 500

<210> 467  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 467  
 Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe  
 1 5 10 15  
 Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr  
 20 25 30  
 Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln  
 35 40 45  
 Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro  
 50 55 60  
 Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr  
 65 70 75 80  
 Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln His Ile Arg Thr Ser  
 85 90 95  
 Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu  
 100 105 110  
 Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile  
 115 120 125  
 Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile Cys  
 130 135 140

<210> 468  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 468

Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val  
1 5 10 15  
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile  
20 25 30  
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys  
35 40 45  
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly  
50 55 60  
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr  
65 70 75 80  
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly  
85 90 95  
Trp Trp Thr Gln  
100

<210> 469

<211> 119

<212> PRT

<213> Homo sapiens

<400> 469

Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly  
1 5 10 15  
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro  
20 25 30  
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu  
35 40 45  
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp  
50 55 60  
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu  
65 70 75 80  
Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala  
85 90 95  
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys  
100 105 110  
Arg Asn Arg Ala Trp His Lys  
115

<210> 470

<211> 140

<212> PRT

<213> Homo sapiens

<400> 470

Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu  
1 5 10 15  
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg  
20 25 30  
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr  
35 40 45  
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln  
50 55 60  
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr  
65 70 75 80  
Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro  
85 90 95  
Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr



Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr  
           35                  40                  45  
 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala  
       50                  55                  60  
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val  
   65                  70                  75                  80  
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala  
                   85                  90                  95  
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala  
                   100                  105                  110  
 Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly  
       115                  120                  125  
 Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val  
       130                  135                  140

<210> 474  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 474  
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala  
   1                  5                  10                  15  
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg  
                   20                  25                  30  
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ala Ala Ala  
       35                  40                  45  
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu  
       50                  55                  60  
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu  
   65                  70                  75                  80  
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg  
                   85                  90                  95  
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val  
                   100                  105                  110  
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg  
       115                  120                  125  
 Pro Gly Ile His Leu Cys  
       130

<210> 475  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 475  
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala  
   1                  5                  10                  15  
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg  
                   20                  25                  30  
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ser Ala Ala  
       35                  40                  45  
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu  
       50                  55                  60  
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu  
   65                  70                  75                  80  
 Ser Gly Pro Arg Gly Pro Thr Cys Arg Ser Phe Ala Val His Thr Arg  
                   85                  90                  95

Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val  
                   100                  105                  110  
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg  
                   115                  120                  125  
 Pro Gly Ile His Leu Cys  
                   130

<210> 476  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 476  
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala Gly  
 1                  5                  10                  15  
 Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro Gln  
                   20                  25                  30  
 Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr  
                   35                  40                  45  
 Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu  
                   50                  55                  60  
 Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala  
 65                  70                  75                  80  
 Ser Gly Arg Ser Pro  
                   85

<210> 477  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 477  
 Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu  
 1                  5                  10                  15  
 Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe  
                   20                  25                  30  
 Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His  
                   35                  40                  45  
 Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val  
                   50                  55                  60  
 Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val  
 65                  70                  75                  80  
 Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu  
                   85                  90                  95  
 Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile  
                   100                  105                  110  
 Leu Ala Thr Leu  
                   115

<210> 478  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 478  
 Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu  
 1                  5                  10                  15  
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe

20 25 30  
 Phe Glu Tyr Leu Glu Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser  
 35 40 45  
 Ala Lys Ser His His Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala  
 50 55 60  
 Ala Pro Leu Leu Ser Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn  
 65 70 75 80  
 Gly Leu Gly Lys Cys His Asp Pro His Phe Thr Gly Glu Glu Thr Glu  
 85 90 95  
 Ala Gln Arg Gly Lys Leu Thr Thr  
 100

<210> 479  
 <211> 439  
 <212> PRT  
 <213> Homo sapiens

<400> 479  
 Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln Leu  
 1 5 10 15  
 Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln Arg  
 20 25 30  
 Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr Asn  
 35 40 45  
 Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys  
 50 55 60  
 Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn Gln  
 65 70 75 80  
 Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro Glu  
 85 90 95  
 Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser Ala  
 100 105 110  
 His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly Ala  
 115 120 125  
 Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile Leu  
 130 135 140  
 Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile Tyr  
 145 150 155 160  
 Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr Ile  
 165 170 175  
 Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys Tyr  
 180 185 190  
 Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn Cys  
 195 200 205  
 Leu Glu Gly Thr His Glu Phe Glu Ala Ile Gly Phe Gln Lys Val  
 210 215 220  
 Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val Leu  
 225 230 235 240  
 Ser Glu Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys Glu  
 250 255  
 Gln Leu Leu Ala Ala Pro Val Arg Ala Lys Leu Asp Arg Gln Arg  
 260 265 270  
 Arg Val Phe Gln Pro Ser Ala Ser Gln Phe Glu Leu Pro Gly  
 275 285  
 Asp Phe Phe Asn Leu Thr Ala Glu Lys Arg Glu Gln Arg Leu  
 290 295 300  
 Arg Ser Glu Ala Val Glu Arg Leu Ser Val Thr Lys Ala Met  
 305 310 315 320

Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu  
 325 330 335  
 Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr  
 340 345 350  
 Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu  
 355 360 365  
 Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys  
 370 375 380  
 Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro  
 385 390 395 400  
 Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile  
 405 410 415  
 Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu  
 420 425 430  
 Ser Ala Ile Glu Lys Leu Leu  
 435

<210> 480  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu  
 1 5 10 15  
 Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala  
 20 25 30  
 Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys  
 35 40 45  
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly  
 50 55 60  
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg  
 65 70 75 80  
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val  
 85 90 95  
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Ser Asp Lys Asn Asn  
 100 105 110  
 Tyr Thr Ser Gly  
 115

<210> 481  
 <211> 171  
 <212> PRT  
 <213> Homo sapiens

<400> 481  
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly  
 1 5 10 15  
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe  
 20 25 30  
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg  
 35 40 45  
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr  
 50 55 60  
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val  
 65 70 75 80  
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His  
 85 90 95

Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	Glu	Asp	Ala	Ile	Arg
			100					105					110		
Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	Lys	Phe	Arg	Lys	Thr
		115					120					125			
Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	Val	Leu	Leu	Ala	Tyr
		130				135					140				
Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	Gly	Met	Asn	Phe	Ile
145					150					155					160
Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Glu					
			165						170						

<210> 482

<211> 177

<212> PRT

<213> Homo sapiens

<400> 482

Met	Gln	Pro	Ala	Glu	Arg	Ser	Arg	Val	Pro	Arg	Ile	Asp	Pro	Tyr	Gly
1				5					10					15	
Phe	Glu	Arg	Pro	Glu	Asp	Phe	Asp	Asp	Ala	Ala	Tyr	Glu	Lys	Phe	Phe
			20					25					30		
Ser	Ser	Tyr	Leu	Val	Thr	Leu	Thr	Arg	Arg	Ala	Ile	Lys	Trp	Ser	Arg
		35					40					45			
Leu	Leu	Gln	Gly	Gly	Gly	Val	Pro	Arg	Ser	Arg	Thr	Val	Lys	Arg	Tyr
		50				55					60				
Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala	Arg	Val	Trp	Met	Val
65					70				75						80
Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	Pro	Gly	Tyr	Tyr	His
			85					90						95	
Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	Glu	Asp	Ala	Ile	Arg
			100					105					110		
Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	Lys	Phe	Arg	Lys	Thr
		115					120					125			
Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	Val	Leu	Leu	Ala	Tyr
		130				135					140				
Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	Gly	Met	Asn	Phe	Ile
145					150					155					160
Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp	Lys	Asn	Leu	Phe	Gly
			165						170						175

Cys